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      M P S R C H                      (TM)

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MPsrch_pp    protein - protein database search, using Smith-Waterman algorithm

Run on:         Tue Mar  3 11:19:37 1998;  MasPar time 2.63 Seconds
                                58.067 Million cell updates/sec

Tabular output not generated.

Title:         >US-08-137-117D-117
Description:   (1-11) from US08137117D.pep
Perfect Score: 70
Sequence:      1 RASQDISSYLN 11

Scoring table:  PAM 150
                Gap 15

Searched:       111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:       a-geneseq30
                1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                14:part14 15:part15 16:part16 17:part17 18:part18
                19:part19 20:part20 21:part21 22:part22 23:part23

Statistics:     Mean 17.502; Variance 52.635; scale 0.333

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	70	100.0	126	5	R29015	pUC-RV1-PM1a.	4.74e-01
2	70	100.0	126	5	R29013	pUC-RVh-PM1a.	4.74e-01
3	70	100.0	127	5	R28670	pPM-k3 protein produc	4.74e-01
4	67	95.7	108	20	W00834	Variable light chain	1.05e+00
5	67	95.7	108	20	W04177	Variant variable ligh	1.05e+00
6	67	95.7	109	17	R52039	Light chain variable	1.05e+00
7	67	95.7	127	22	W11815	Mouse anti-human Fas	1.05e+00
8	67	95.7	127	22	W11817	Humanised mouse anti-	1.05e+00
9	67	95.7	127	5	R29010	p146-k3 protein produ	1.05e+00
10	67	95.7	131	14	R84553	MAb SCH94.03 light ch	1.05e+00
11	67	95.7	268	8	R44226	Chimeric Ig superfami	1.05e+00
12	67	95.7	273	9	R52865	Anti-influenza N10 sc	1.05e+00
13	66	94.3	128	5	R09426	ME4 Light Chain V Reg	1.37e+00
14	66	94.3	128	19	W06215	MAb ME4 light chain v	1.37e+00
15	64	91.4	11	20	W13920	Fragment of CDR-1 of	2.31e+00
16	64	91.4	95	12	R72058	KI012 VK region.	2.31e+00
17	64	91.4	95	12	R72065	S43434 VK-1 region.	2.31e+00
18	64	91.4	107	10	R54260	Anti-HIV gp120 immuno	2.31e+00
19	64	91.4	107	19	W01284	VL region of HIV neut	2.31e+00
20	64	91.4	107	19	W01283	VL region of HIV neut	2.31e+00
21	64	91.4	107	10	R54261	Anti-HIV gp120 immuno	2.31e+00
22	64	91.4	108	23	W13521	Anti-melanoma light c	2.31e+00
23	64	91.4	108	23	W13530	Anti-melanoma light c	2.31e+00
24	64	91.4	113	20	W13924	Light chain #2 for an	2.31e+00
25	64	91.4	114	20	W13922	Light chain #1 for an	2.31e+00
26	64	91.4	127	7	R39265	Mouse C4G1 Ig light-c	2.31e+00
27	64	91.4	132	22	W22842	Human anti-tumour ant	2.31e+00
28	64	91.4	214	6	R30776	H52L6-158 murine anti	2.31e+00
29	64	91.4	214	19	R43338	Completely humanised	2.31e+00
30	64	91.4	214	19	W00373	Anti-CD18 chimeric an	2.31e+00
31	64	91.4	233	6	R30777	pH52-9.0 humanised mu	2.31e+00
32	63	90.0	104	19	W01285	VL region of HIV neut	3.00e+00
33	63	90.0	104	19	R54318	Anti-HIV gp120 immuno	3.00e+00
34	63	90.0	107	7	R41283	Moderate-risk modifie	3.00e+00
35	63	90.0	107	7	R38614	Low-risk modified (pr	3.00e+00
36	63	90.0	109	6	R30764	Consensus humanised a	3.00e+00
37	63	90.0	109	9	R47041	Sequence of the conse	3.00e+00
38	63	88.6	127	19	R99003	MAb VL17E6 light chai	3.89e+00
39	62	88.6	11	17	R52523	Gloop2 light chain c	3.89e+00
40	62	88.6	104	9	R54322	Anti-HIV gp120 immuno	3.89e+00
41	62	88.6	107	6	R30769	huxCD3v9, humanised m	3.89e+00
42	62	88.6	107	6	R30768	Murine anti-CD3 MAb U	3.89e+00
43	62	88.6	108	4	R21286	Murine VL kappa group	3.89e+00
44	62	88.6	108	10	R54062	Anti-cancer monoclona	3.89e+00
45	62	88.6	128	5	R29579	CLN-IgG kappa.	3.89e+00

ALIGNMENTS

```
RESULT     1
ID   R29015 standard; Protein; 126 AA.
AC   R29015;
DT   30-MAR-1993  (first entry)
DE   pUC-RV1-PM1a.
KW   Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW   complementarity determining region; mouse; monoclonal; hybridoma;
KW   plasmid; polymerase chain reaction; amplify.
OS   Synthetic.
FH   Key               Location/Qualifiers
FT   Peptide           1..19
FT   /note= "Leader peptide"
FT   Region            20..42
FT   /label= FR1
FT   Region            43..53
FT   /label- CDR1
FT   Region            54..68
FT   /label= FR2
FT   Region            69..75
FT   /label= CDR2
FT   Region            76..107
FT   /label= FR3
FT   Region            108..116
FT   /label= CDR3
FT   Region            117..126
FT   /label- FR4
PN   WO9219759-A.
PD   12-NOV-1992.
PF   24-APR-1992; J00544.
PR   25-APR-1991; JP-095476.
PR   19-FEB-1992; JP-032084.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR   WPI; 92-398882/48.
DR   N-PSDB; Q31366.
PT   Reconstituted human antibody to human interleukin-6 receptor -
PT   has low antigenicity and contains mouse V-region complementarity
PT   determining regions
PS   Disclosure: Page 144-5; 207pp; Japanese.
CC   The sequences given in R29012-15 are portions of monoclonal antibodies
CC   which were encoded by plasmids derived from mouse hybridomas. The DNA
CC   encoding complementarity determining regions (CDR's) was isolated by
CC   polymerase chain reaction. These antibodies recognise human
CC   interleukin-6 receptor (IL-6R).  The mouse hybridoma cells were
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CC    transformed with the plasmids encoding these genes which caused the
CC    secretion of these antibodies from the hybridoma cells.
SQ    Sequence  126 AA;

Query Match          100.0%;       Score 70;  DB 5; Length 126;
Best Local Similarity 100.0%;      Pred. No. 4.74e-01;
Matches   11; Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    43 rasqdissyln 53
         |||||||||||
Qy     1 RASQDISSYLN 11

RESULT  2
ID   R29013 standard; Protein; 126 AA.
AC   R29013;
DT   30-MAR-1993 (first entry)
DE   pUC-RVh-PM1a.
KW   Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW   complementarity determining region; mouse; monoclonal; hybridoma;
KW   plasmid; polymerase chain reaction; amplify.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT   /note= "Leader peptide"
FT   Region          20..42
FT   /label- FR1
FT   Region          43..53
FT   /label- CDR1
FT   Region          54..68
FT   /label- FR2
FT   Region          69..75
FT   /label- CDR2
FT   Region          76..107
FT   /label- FR3
FT   Region          108..116
FT   /label- CDR3
FT   Region          117..126
FT   /label- FR4
PN   WO9219759-A.
PD   12-NOV-1992.
PF   24-APR-1992; J00544.
PR   25-APR-1991; JP-095476.
PR   19-FEB-1992; JP-032084.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR   WPI; 92-398882/48.
DR   N-PSDB; Q31361.
PT   Reconstituted human antibody to human interleukin-6 receptor -
PT   has low antigenicity and contains mouse V-region complementarity
PT   determining regions
PS   Disclosure; Page 140-1; 207pp; Japanese.
CC   The sequences given in R29012-15 are portions of monoclonal antobodies
CC   which were encoded by plasmids derived from mouse hybridomas. The DNA
CC   encoding complementarity determining regions (CDR's) was isolated by
CC   polymerase chain reaction.  These antibodies recognise human
CC   interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
CC   transformed with the plasmids encoding these genes which caused the
CC   secretion of these antibodies from the hybridoma cells.
SQ   Sequence  126 AA;

Query Match          100.0%;       Score 70;  DB 5; Length 126;
Best Local Similarity 100.0%;      Pred. No. 4.74e-01;
Matches   11; Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    43 rasqdissyln 53
         |||||||||||
Qy     1 RASQDISSYLN 11

RESULT  3
ID   R28670 standard; Protein; 127 AA.
AC   R28670;
DT   30-MAR-1993 (first entry)
DE   pPM-k3 protein product.
KW   Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW   heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
KW   plasmid; pPM-k3; pPM-h1.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT   /note= "Signal peptide"
FT   Protein         21..127
FT   /note= "Mature peptide"
PN   WO9219759-A.
PD   12-NOV-1992.
PF   24-APR-1992; J00544.
PR   25-APR-1991; JP-095476.
PR   19-FEB-1992; JP-032084.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR   WPI; 92-398882/48.
DR   N-PSDB; Q30755.
PT   Reconstituted human antibody to human interleukin-6 receptor -
PT   has low antigenicity and contains mouse V-region complementarity
PT   determining regions
PS   Disclosure; Page 121-122; 207pp; Japanese.
CC   The sequences given in R28670-71 were encoded by plasmids which were
CC   used in example to illustrate the production of a human antibody which
CC   recognises human interleukin-6 receptor (IL-6R).  The antibody
CC   comprises light (L) chain and heavy (H) chain variable regions which
CC   were derived from a mouse monoclonal antibody produced from the
CC   hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1.
SQ   Sequence  127 AA;

Query Match          100.0%;       Score 70;  DB 5; Length 127;
Best Local Similarity 100.0%;      Pred. No. 4.74e-01;
Matches   11; Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    44 rasqdissyln 54
         |||||||||||
Qy     1 RASQDISSYLN 11

RESULT  4
ID   W00834 standard; Protein; 108 AA.
AC   W00834;
DT   20-MAY-1997 (first entry)
DE   Variable light chain of anti-human Fas ligand antibody NOK-1.
KW   Variable light region; light chain; human; Fas ligand; monoclonal;
KW   antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;
KW   diagnosis; disease; hepatitis; infectious mononucleosis;
KW   systemic lupus erythematosus.
OS   Mus musculus.
PN   WO9629350-A1.
PD   26-SEP-1996.
PF   21-MAR-1996; J00734.
PR   21-MAR-1996; JP-087420.
PR   27-OCT-1995; JP-303492.
PA   (SUME ) SUMITOMO ELECTRIC IND CO.
PI   Kayagaki N, Nakata M, Okumura K, Yagita H;
DR   WPI; 96-443140/44.
DR   N-PSDB; T39560.
PT   Monoclonal antibody specifically recognising the Fas ligand - useful
PT   for the detection of Fas ligands either on cell surface or in
PT   solution
PS   Claim 41; Pages 93-94; 133pp; Japanese.
CC   The present sequence is the light chain variable region of the
CC   anti-human Fas ligand monoclonal antibody (MAb) NOK-1. NOK-1 is
CC   produced by the hybridoma NOK-1 (FERM BP-5044), which was prepared
CC   by immunising mice with transformed human Fas ligand expressing COS
CC   cells, and fusing spleen cells isolated from the mice with myeloma
CC   P3x63Ag8.653 (ATCC CRL-1580) cells. The MAb recognises the human
CC   Fas ligand on the cell surface or in solution, and can be used to
CC   inhibit the apoptosis inducing cell surface Fas ligand/Fas
CC   reaction. The MAb can also be used for a Fas ligand assay in
```

CC   biological samples (e.g. human blood), especially for disease
CC   diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
CC   lupus erythematosus.
SQ   Sequence 108 AA;

Query Match   95.7%; Score 67; DB 20; Length 108;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   24 rasqdisnyln 34
          ||||||:||
Qy   1 RASQDISSYLN 11

RESULT 5
ID   W04177 standard; Protein; 108 AA.
AC   W04177;
DT   19-MAY-1997 (first entry)
DE   Variant variable light chain of Fas ligand antibody NOK-1.
KW   Variable region; light chain; human; Fas ligand; monoclonal;
KW   antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;
KW   diagnosis; disease; hepatitis; infectious mononucleosis; variant.
OS   Mus musculus.
PN   WO9629350-A1.
PD   26-SEP-1996.
PF   21-MAR-1996; J00734.
PR   20-MAR-1995; JP-087420.
PR   27-OCT-1995; JP-303492.
PA   (SUME) SUMITOMO ELECTRIC IND CO.
PI   Kayagaki N, Nakata M, Okumura K, Yagita H;
DR   WPI; 96-443140/44.
DR   N-PSDB; T39550.
PT   Monoclonal antibody specifically recognising the Fas ligand - useful
PT   for the detection of Fas ligands either on cell surface or in
PT   solution
PS   Claim 20; Pages 80-81; 133pp; Japanese.
CC   The present sequence is a variant light chain variable region
CC   of the anti-human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1
CC   is produced by the hybridoma NOK-1 (FERM BP-5044), which was
CC   prepared by immunising mice with transformed human Fas ligand
CC   expressing COS cells, and fusing spleen cells isolated from the
CC   mice with myeloma P3x63Ag8.653 (ATCC CRL-1580) cells. The MAb
CC   recognises the human Fas ligand on the cell surface or in solution,
CC   and can be used to inhibit the apoptosis inducing cell surface Fas
CC   ligand/Fas reaction. The MAb can also be used for a Fas ligand
CC   assay in biological samples (e.g. human blood), especially for
CC   disease diagnosis, e.g. hepatitis, infectious mononucleosis and
CC   systemic lupus erythematosus.
SQ   Sequence 108 AA;

Query Match   95.7%; Score 67; DB 20; Length 108;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   24 rasqdisnyln 34
          ||||||:||
Qy   1 RASQDISSYLN 11

RESULT 6
ID   R52039 standard; Protein; 109 AA.
AC   R52039;
DT   27-SEP-1996 (first entry)
DE   Light chain variable region of murine antibody 1f19.
KW   antibody; humanised; murine; human; heavy chain; light; variable;
KW   framework region; complementarity determining region; reshaping;
KW   modelling; surface residue; modify.
OS   Mus sp.
FH   Key   Location/Qualifiers
FT   Region   1..23
FT   /label= framework_region_1
FT   /note= "FR 1"
FT   Region   24..34
FT   /label= complementarity_determining_region_1
FT   /note= "CDR 1"
FT   Region   35..49
FT   /label- FR_2
FT   Region   50..56
FT   /label- CDR_2
FT   Region   57..88
FT   /label- FR_3
FT   Region   89..97
FT   /label- CDR_3
FT   Region   98..109
FT   /label- FR_4
PN   EP-592106-A1.
PD   13-APR-1994
PF   07-SEP-1993; 307051.
PR   09-SEP-1992; US-942245.
PA   (PEDE/) PEDERSEN J T.
PA   (IMMU-) IMMUNOGEN INC.
PI   Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
DR   WPI; 94-120230/15.
PT   Method of resurfacing of rodent antibodies to produce humanised
PT   antibody forms - for producing non-human antibodies with improved
PT   therapeutic efficiency by presenting human surface on V-region
PS   Example 1; Fig 3A; 230pp; English.
CC   The present sequence is that of the light chain variable (LC VR) region
CC   of murine antibody 1f19. This sequence was aligned with 11 other known
CC   antibody LC VRs and a set of framework positions of surface exposed amino
CC   acid residues was determined. This information can be used in a method to
CC   determine how to modify a rodent antibody or fragment by resurfacing in
CC   order to produce a humanised rodent antibody. Residues (determined from
CC   alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
CC   87, 111, 115, 116 and 117 are accessible residues. None of the entire
CC   combinations of surface residues in the murine sequences were found in
CC   the human sequences and vice versa. However the residues in individual
CC   positions appear to be conserved.
SQ   Sequence 109 AA;

Query Match   95.7%; Score 67; DB 17; Length 109;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   24 rasqdisnyln 34
          ||||||:|||
Qy   1 RASQDISSYLN 11

RESULT 7
ID   W11815 standard; Protein; 127 AA.
AC   W11815;
DT   20-OCT-1997 (first entry)
DE   Mouse anti-human Fas ligand antibody F919 light chain.
KW   Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
KW   induction; assay; enzyme linked immunosorbant assay; diagnosis;
KW   disease; hepatitis B; hepatitis C; human immunodeficiency virus;
KW   graft versus host disease; ulcerative colitis; sequelae;
KW   myocardial infarction; mouse; murine; monoclonal; treatment;
KW   complementarity determining region; CDR.
OS   Mus spp.
FH   Key   Location/Qualifiers
FT   Region   44..54
FT   /label- CDR_1
FT   Region   70..76
FT   /label- CDR_2
FT   Region   109..117
FT   /label- CDR_3
PN   WO9702290-A1.
PD   23-JAN-1997.
PF   01-JUL-1996; J01820.
PR   17-MAY-1996; US-649100.
PR   30-JUN-1995; JP-188480.
PA   (MOCH) MOCHIDA PHARM CO LTD.
PA   (OSAB-) OSAKA BIOSCIENCE INST.

PI   Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
DR   WPI; 97-108917/10.
DR   N-PSDB; T59500.
PT   Antibody reactive with Fas ligand capable of inducing apoptosis -
PT   used for diagnostic assay of Fas ligand in body fluids and for
PT   treatment of diseases in which Fas ligand/Fas antigen is involved
PS   Claim 5; Fig 10; 164pp; Japanese.
CC   The present sequence is the light chain of the mouse
CC   anti-apoptosis inducing human Fas ligand, monoclonal antibody,
CC   F919. The antibody can be used in a Fas ligand assay, e.g. an
CC   enzyme linked immunosorbant assay, to diagnose diseases in which
CC   the Fas ligand/Fas antigen system is implicated, e.g. hepatitis
CC   B/C, human immunodeficiency virus, graft/host disorders,
CC   ulcerative colitis or sequelae of myocardial infarction. The
CC   antibody may also be used to treat such diseases.
SQ   Sequence 127 AA;

Query Match   95.7%; Score 67; DB 22; Length 127;
Best Local Similarity   90.9%; Pred. No. 1.05e+00;
Matches   10; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   44 rasqdisnyln 54
              ||||||:|||
Qy   1 RASQDISSYLN 11

RESULT   8
ID   W11817 standard; Protein; 127 AA.
AC   W11817;
DT   20-OCT-1997 (first entry)
DE   Humanised mouse anti-human Fas ligand antibody F919 light chain.
KW   Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
KW   induction; assay; enzyme linked immunosorbant assay; diagnosis;
KW   disease; hepatitis B; hepatitis C; human immunodeficiency virus;
KW   graft versus host disease; ulcerative colitis; sequelae; chimeric;
KW   myocardial infarction; mouse; murine; monoclonal; treatment.
OS   Chimeric - Mus spp.
OS   Chimeric - Homo sapiens.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   Region   44..54
FT   /label- CDR_1
FT   Region   70..76
FT   /label- CDR_2
FT   Region   109..117
FT   /label- CDR_3
PN   WO9702290-A1.
PD   23-JAN-1997.
PF   01-JUL-1996; J01820.
PR   17-MAY-1996; US-649100.
PR   30-JUN-1995; JP-188480.
PA   (MOCH) MOCHIDA PHARM CO LTD.
PA   (OSAB-) OSAKA BIOSCIENCE INST.
PI   Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
DR   WPI; 97-108917/10.
DR   N-PSDB; T59502.
PT   Antibody reactive with Fas ligand capable of inducing apoptosis -
PT   used for diagnostic assay of Fas ligand in body fluids and for
PT   treatment of diseases in which Fas ligand/Fas antigen is involved
PS   Claim 5; Fig 12; 164pp; Japanese.
CC   The present sequence is the light chain of the humanised
CC   mouse anti-apoptosis inducing human Fas ligand, monoclonal
CC   antibody, F919. The antibody can be used in a Fas ligand assay,
CC   e.g. an enzyme linked immunosorbant assay, to diagnose diseases
CC   in which the Fas ligand/Fas antigen system is implicated, e.g.
CC   hepatitis B/C, human immunodeficiency virus, graft/host disorders,
CC   ulcerative colitis or sequelae of myocardial infarction. The
CC   antibody may also be used to treat such diseases.
SQ   Sequence 127 AA;

Query Match   95.7%; Score 67; DB 22; Length 127;
Best Local Similarity   90.9%; Pred. No. 1.05e+00;
Matches   10; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db   44 rasqdisnyln 54
              ||||||:|||
Qy   1 RASQDISSYLN 11

RESULT   9
ID   R29010 standard; Protein; 127 AA.
AC   R29010;
DT   30-MAR-1993 (first entry)
DE   p146-k3 protein product.
KW   Human; antibody; interleukin-6; receptor; IL-6R; light chain; L: H:
KW   heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
KW   plasmid; p146-k3; p146-hl.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   Peptide   1..20
FT   /note- "Signal peptide"
FT   Protein   21..127
FT   /note- "Mature peptide"
PN   WO9219759-A.
PD   12-NOV-1992.
PF   24-APR-1992; J00544.
PR   25-APR-1991; JP-095476.
PR   19-FEB-1992; JP-032084.
PA   (CHUS) CHUGAI SEIYAKU KK.
PI   Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR   WPI; 92-398882/48.
DR   N-PSDB; Q30759.
PT   Reconstituted human antibody to human interleukin-6 receptor -
PT   has low antigenicity and contains mouse V-region complementarity
PT   determining regions
PS   Disclosure; Page 127-128; 207pp; Japanese.
CC   The sequences given in R29010-11 were encoded by plasmids which were
CC   used in example to illustrate the production of a human antibody which
CC   recognises human interleukin-6 receptor (IL-6R). The antibody
CC   comprises light (L) chain and heavy (H) chain variable regions which
CC   were derived from a mouse monoclonal antibody produced from the
CC   hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-hl.
SQ   Sequence 127 AA;

Query Match   95.7%; Score 67; DB 5; Length 127;
Best Local Similarity   90.9%; Pred. No. 1.05e+00;
Matches   10; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   44 rasqdisnyln 54
              ||||||||:|||
Qy   1 RASQDISSYLN 11

RESULT   10
ID   R84553 standard; Protein; 131 AA.
AC   R84553;
DT   02-FEB-1996 (first entry).
DE   MAb SCH94.03 light chain.
KW   Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system;
KW   CNS; demyelination; multiple sclerosis; neural disease; therapeutic.
OS   Mus sp.
FH   Key   Location/Qualifiers
FT   Peptide   1..20
FT   /label- Leader_peptide
FT   Region   44..54
FT   /label- CDR1
FT   Region   70..76
FT   /label- CDR2
FT   Region   109..117
FT   /label- CDR3
FT   Region   116..128
FT   /label- Joining_region
FT   Region   129..131
FT   /label- C-kappa_region
PN   WO9530004-Al.
PD   09-NOV-1995.

```
PF
PR    27-APR-1995; U05262.
PR    29-APR-1994; US-236520.
PA    (MAYO-) MAYO FOUNDATION.
PI    Miller DJ, Rodriguez M;
DR    WPI: 95-393077/50.
DR    N-PSDB; T05311.
PT    Monoclonal antibodies which stimulate central nervous system
PT    re-myelination - are produced by hybridoma ATCC CRL 11627, for
PT    treating multiple sclerosis, and viral or post-neural diseases of
PT    the CNS.
PS    Disclosure; Page 36-37; 63pp; English.
CC    Hybridoma ATCC CRL 11627 was obtd. from a SJL/J mouse injected with
CC    spinal cord homogenate from a mammal uninfected with any
CC    demyelinating disease. The hybridoma produced a monoclonal antibody
CC    (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
CC    light chain amino acid sequence is given in R84553.
SQ    Sequence 131 AA;

Query Match       95.7%;    Score 67;  DB 14;  Length 131;
Best Local Similarity  90.9%;  Pred. No. 1.05e+00;
Matches 10;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db    44 rasqdisnyln 54
          |||||||:|||
Qy     1 RASQDISSYLN 11

RESULT 11
ID    R44226 standard; protein; 268 AA.
AC    R44226;
DT    10-JUN-1994 (first entry)
DE    Chimeric Ig superfamily protein analogue R19(D1.3).
KW    CHI-protein; Immunoglobulin superfamily; multivalent antigen binding;
KW    engineered fusion protein; beta-barrel domain; chimaeric;
KW    complementarity determining region; cell imaging; targetting.
OS    Synthetic.
FH    Key        Location/Qualifiers
FT    Region     1..30
FT    /label= H_FR1
FT    /note= "Heavy chain framework region from R19.9"
FT    Region     31..35
FT    /label- H1
FT    /note= "primary CDR loop from R19.9"
FT    Region     36..39
FT    /label- FR2A
FT    /note= "Heavy chain framework region from R19.9"
FT    Region     40..45
FT    /label- H3'
FT    /note- "CDR loop spliced into chi-site from D1.3"
FT    Region     46..48
FT    /label- FR2B
FT    /note= "Heavy chain framework region from R19.9"
FT    Region     49..65
FT    /label- H2
FT    /note= "primary CDR loop from R19.9"
FT    Region     66..89
FT    /label- H_FR3A
FT    /note= "Heavy chain framework region from R19.9"
FT    Region     90..92
FT    /label- H1'
FT    /note- "CDR loop spliced into chi-site from D1.3"
FT    Region     93..97
FT    /label- H_FR3B
FT    /note= "Heavy chain framework region from R19.9"
FT    Region     98..112
FT    /label- H3
FT    /note= "primary CDR loop from R19.9"
FT    Region     113..116
FT    /label- H_FR4
FT    /note= "Heavy chain framework region from R19.9"
FT    Region     117..135
FT    /label- H2'
FT    /note- "CDR loop spliced into chi-site from D1.3"
```

```
FT    Region     136..155
FT    /label=
FT    /note= "bridge/linker"
FT    Region     156..178
FT    /label- L_FR1
FT    /note= "light chain framework region from R19.9"
FT    Region     179..189
FT    /label- L1
FT    /note= "primary CDR loop from R19.9"
FT    Region     190..193
FT    /label- FR2A
FT    /note= "Light chain framework region from R19.9"
FT    Region     194..199
FT    /label- L3'
FT    /note- "CDR loop spliced into chi-site from D1.3"
FT    Region     200..203
FT    /label- FR2B
FT    /note= "Light chain framework region from R19.9"
FT    Region     204..210
FT    /label- L2
FT    /note= "primary CDR loop from R19.9"
FT    Region     211..237
FT    /label- L_FR3A
FT    /note= "Light chain framework region from R19.9"
FT    Region     238..241
FT    /label- L1'
FT    /note- "CDR loop spliced into chi-site from D1.3"
FT    Region     242..244
FT    /label- FR3B
FT    /note= "Light chain framework region from R19.9"
FT    Region     245..253
FT    /label- L3
FT    /note= "primary CDR loop from R19.9"
FT    Region     254..255
FT    /label- FR4
FT    /note= "Light chain framework region from R19.9"
FT    Region     256..268
FT    /label- L2'
FT    /note- "CDR loop spliced into chi-site from D1.3"
PN    WO9323537-A.
PD    25-NOV-1993.
PF    07-MAY-1993; U04338.
PR    08-MAY-1992; US-881109.
PA    (CREA-) CREATIVE BIOMOLECULES.
PI    Huston JS, Keck PC;
DR    WPI; 93-386569/48.
PT    Chimeric multivalent protein analogues - useful for diagnostic
PT    imaging and cytotoxic therapy
PS    Example 1; Fig 14; 106pp; English.
CC    This sequence is an example of a CHI-protein constructed according
CC    to the invention. The novel CHI (Chimeric Immunoglobulin)-proteins
CC    are comprised of at least 1 beta-barrel forming domain. The antigen
CC    binding sites of the molecule are located in the beta-barrel
CC    domain(s). Splice sites for insertion of specific binding sites are
CC    located by computer comparisons of homology and structure. Depending
CC    on the ligand binding specificity of the chimeric molecules, they
CC    can be targetted for imaging, irradiating or delivering cytotoxic
CC    substances to specific tissues.
SQ    Sequence 268 AA;

Query Match       95.7%;    Score 67;  DB 8;  Length 268;
Best Local Similarity  90.9%;  Pred. No. 1.05e+00;
Matches 10;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db    179 rasqdisnyln 189
           |||||||:|||
Qy      1 RASQDISSYLN 11

RESULT 12
ID    R52865 standard; Protein; 273 AA.
AC    R52865;
DT    09-SEP-1994 (first entry)
DE    Anti-influenza N10 scFv.
```

KW Monoclonal antibody N10; target binding polypeptide; scFv;
KW scFv; single chain antibody; protein secretion; FLAG;
KW Escherichia coli; antibody engineering; humanized antibody;
KW influenza virus; neuraminidase.
OS Not specified.
FH Key   Location/Qualifiers
FT Peptide   1..22
FT /label= Sig_peptide
FT Peptide   266..273
FT /note= "C-terminal FLAG tail"
PN WO9407921-A.
PD 14-APR-1994.
PF 24-SEP-1993; AU04491.
PR 25-SEP-1992; AU-004973.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
PI Lah M, Malbyrl, Power BE;
DR WPI; 94-135515/16.
DR P-PSDB; Q62957.
PT New target-binding polypeptide(s) used for diagnosis, etc. -
PT having a stable core polypeptide region with at least one
PT target-binding region covalently attached, opt. mutated to alter
PT specificity, etc.
PS Disclosure; Page 41; 67pp; English.
CC An scFv fragment of NC10 (a monoclonal antibody that recognises
CC influenza virus N9 neuraminidase) was expressed in Escherichia
CC coli. The N-terminal PelB signal peptide directed the scFv
CC fragment into the periplasm where it became associated with the
CC insoluble membrane fraction. An octapeptide FLAG tail was fused to
CC the C-terminus of scFv and used to monitor scFv during
CC purification.
SQ Sequence   273 AA;

Query Match   95.7%;   Score 67; DB 9; Length 273;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db   182 rasqdisnyln 192
           |||||||::|||
Qy   1 RASQDISSYLN 11

RESULT 13
ID R09426 standard; Protein; 128 AA.
AC R09426;
DT 04-MAR-1993 (first entry)
DE ME4 Light Chain V Region (mouse)
KW Monoclonal antibody; chimera; light; heavy; chain; constant;
KW variable; antigen; diagnosis; cancer; tumour.
OS Mus musculus.
PN WO9002569-A.
PD 22-MAR-1990.
PF 06-SEP-1989; U03852.
PR 06-SEP-1988; US-240624.
PR 08-SEP-1988; US-241744.
PR 13-SEP-1988; US-243739.
PR 04-OCT-1988; US-253002.
PR 19-JUN-1989; US-367641.
PR 21-JUL-1989; US-382768.
PA (ITGE-) INT GENETIC ENG INC.
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
DR WPI; 90-115825/15.
DR N-PSDB; Q08608.
PT Chimeric mouse-human antibodies - prepd. using genes coding for
PT constant human region murine variable region, esp. to 3 tumour
PT antigen
PS Claim 13; Page 123 + Fig 29; 173pp; English.
CC The sequence is used in the prodn. of a chimeric antibody mol.
CC comprising two light chains and two heavy chains, each having a
CC constant region (human) and a variable region (murine) having
CC specificity to an antigen bound by murine monoclonal antibody
CC (MAb) ME4. The chimeric antibodies can be used for any purpose for
CC which the original murine MAbs can be used, with the advantage that

CC they are more compatible with the human body. They are esp. used for
CC the diagnosis and treatment of cancer.
SQ Sequence   128 AA;

Query Match   94.3%;   Score 66; DB 5; Length 128;
Best Local Similarity 81.8%; Pred. No. 1.37e+00;
Matches   9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db   44 rasqdittyln 54
          |||||::|||
Qy   1 RASQDISSYLN 11

RESULT 14
ID W06215 standard; Protein; 128 AA.
AC W06215;
DT 13-FEB-1997 (first entry)
DE MAb ME4 light chain variable region.
KW Chimeric antibody; monoclonal antibody; ME4; antibody engineering;
KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.
OS Mus sp.
PN US5576184-A.
PD 19-NOV-1996.
PF 06-SEP-1988; 240624.
PR 06-SEP-1988; US-240624.
PR 08-SEP-1988; US-241744.
PR 13-SEP-1988; US-243739.
PR 04-OCT-1988; US-253002.
PR 19-JUN-1989; US-367641.
PR 21-JUL-1989; US-382768.
PR 06-MAY-1991; US-659401.
PR 27-DEC-1994; US-364001.
PA (XOMA) XOMA CORP.
PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
DR WPI; 97-011249/01.
DR N-PSDB; T43440.
PT Chimeric mouse-human antibodies - recognise a human tumour antigen,
PT used for the treatment and diagnosis of human cancers
PS Example 3; Fig 29; 102pp; English.
CC The light chain variable region (W06215) of mouse monoclonal
CC antibody ME4 is the product of a cDNA clone (T43440) isolated
CC from a ME4 hybridoma cDNA library. MAb ME4 (IgG1) binds to an
CC antigen that is expressed on the surface of human lung, breast,
CC colon and ovary carcinomas and melanomas, but not on most normal
CC adult tissues. The light chain and heavy chain variable regions
CC (see also W06216) of ME4 can be linked to human constant regions
CC and expressed in transformed host cells. Novel mouse-human
CC chimeric antibodies (see also W06209-14 and W06217-18) can be
CC produced that have specificity to human tumour antigens for use in
CC the treatment and diagnosis of human cancer.
SQ Sequence   128 AA;

Query Match   94.3%;   Score 66; DB 19; Length 128;
Best Local Similarity 81.8%; Pred. No. 1.37e+00;
Matches   9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db   44 rasqdittyln 54
          |||||::|||
Qy   1 RASQDISSYLN 11

RESULT 15
ID W13920 standard; peptide; 11 AA.
AC W13920;
DT 15-MAY-1997 (first entry)
DE Fragment of CDR-1 of light-chain variable region.
KW Antibody; heavy chain; light chain; variable region; human;
KW complementarity determining region; human; adr type hepatitis B virus;
KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine.
OS Homo sapiens.
PN J09020798-A.
PD 21-JAN-1997.

```
PF    11-JUL-1995; 174752.
PR    11-JUL-1995; JP-174752.
PA    (ASAH ) ASAHI KASEI KOGYO KK.
DR    WPI; 97-140911/13.
DR    N-PSDB: T60115.
PT    Human anti-Hepatitis B antibody - used in a adr type HB virus
      vaccine
PS    Claim 6; Page 2; 20pp; Japanese.
CC    This sequence represents a fragment of the complementarity determining
CC    region-1 (CDR-1) of the light chain variable region of a human
CC    monoclonal antibody of the invention.  The antibody of the invention also
CC    contains the represented by W13912 in the CDR-1 of the heavy chain
CC    variable region.  The antibody is capable of binding to adr type
CC    hepatitis B (HB) virus antigen.  A human anti-HB virus monoclonal
CC    antibody preparation which is highly safe and is effective to adr type HB
CC    virus can be provided, using the monoclonal antibody.  It can also be
CC    used as a vaccine against HB infection.
SQ    Sequence   11 AA;

Query Match      91.4%;  Score 64;  DB 20;  Length 11;
Best Local Similarity   90.9%;  Pred. No. 2.31e+00;
Matches    10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Db     1 rasqsissyln 11
         ||||.|||||||
Qy     1 RASQDISSYLN 11


Search completed: Tue Mar   3 11:19:50 1998
Job time : 13 secs.
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**********
M P S R C H (TM)
**********

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MPsrch_pp  protein - protein database search, using Smith-Waterman algorithm

Run on:        Tue Mar 3 11:19:07 1998;  MasPar time 2.96 Seconds
                                         113.234 Million cell updates/sec

Tabular output not generated.

Title:          >US-08-137-117D-117
Description:    (1-11) from US08137117D.pep
Perfect Score:  70
Sequence:       1 RASQDISSYLN 11

Scoring table:  PAM 150
                Gap 15

Searched:       95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:       pir53
                1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
                8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
                13:unann9 14:unann10 15:unann11 16:unann12 17:unenc
                18:unrev

Statistics:     Mean 23.804;  Variance 32.457;  scale 0.733

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                  SUMMARIES
```

Result No.	Score	Query % Match	Length	DB	ID	Description	Pred. No.
1	68	97.1	105	7	PH0087	Ig kappa chain V reg	3.54e-03
2	67	95.7	93	7	S38564	Ig light chain V reg	5.82e-03
3	67	95.7	107	7	S69906	Ig kappa light chain	5.82e-03
4	67	95.7	107	7	B28044	Ig kappa chain V reg	5.82e-03
5	67	95.7	107	7	B49026	Ig kappa chain V reg	5.82e-03
6	67	95.7	107	7	A28044	Ig kappa chain V reg	5.82e-03
7	67	95.7	107	7	D48677	Ig light chain V-J r	5.82e-03
8	67	95.7	107	7	S69901	Ig kappa light chain	5.82e-03
9	67	95.7	108	7	S38862	Ig kappa chain V reg	5.82e-03
10	67	95.7	108	7	S69903	Ig kappa light chain	5.82e-03
11	67	95.7	108	7	S69902	Ig kappa light chain	5.82e-03
12	67	95.7	108	7	S69900	Ig kappa light chain	5.82e-03
13	67	95.7	108	2	KVMSAR	Ig kappa chain V reg	5.82e-03
14	67	95.7	108	7	C26405	Ig kappa chain V reg	5.82e-03
15	67	95.7	108	7	PL0282	Ig light chain V reg	5.82e-03
16	67	95.7	115	7	A53276	Ig light chain precu	5.82e-03
17	67	95.7	115	7	JL0080	Ig light chain precu	5.82e-03
18	67	95.7	128	7	A26406	Ig kappa chain V reg	5.82e-03
19	65	92.9	109	7	S31981	Ig kappa chain - hum	1.55e-02
20	64	91.4	86	7	S34086	Ig kappa chain V reg	2.53e-02
21	64	91.4	87	7	S34083	Ig kappa chain V reg	2.53e-02
22	64	91.4	87	7	S34084	Ig kappa chain V reg	2.53e-02
23	64	91.4	88	7	S21528	Ig kappa chain V reg	2.53e-02
24	64	91.4	88	7	S21522	Ig kappa chain V reg	2.53e-02
25	64	91.4	92	7	D28840	Ig kappa chain V reg	2.53e-02
26	64	91.4	101	7	B28840	Ig kappa chain V reg	2.53e-02
27	64	91.4	101	7	C28840	Ig kappa chain V reg	2.53e-02
28	64	91.4	107	7	B48677	Ig light chain V-J r	2.53e-02
29	64	91.4	107	7	A48677	Ig light chain V-J r	2.53e-02
30	64	91.4	107	7	S32188	Ig kappa chain V reg	2.53e-02
31	64	91.4	107	7	C46677	Ig light chain V-J r	2.53e-02
32	64	91.4	108	7	S36264	Ig lambda chain v re	2.53e-02
33	64	91.4	108	7	S44122	Ig kappa chain v reg	2.53e-02
34	64	91.4	108	7	S47182	Ig kappa chain - hum	2.53e-02
35	64	91.4	108	7	B26405	Ig kappa chain V reg	2.53e-02
36	64	91.4	108	7	B49047	IgM monoclonal stria	2.53e-02
37	64	91.4	116	7	A27594	Ig kappa chain precu	2.53e-02
38	64	91.4	117	7	S24206	Ig kappa chain V reg	2.53e-02
39	64	91.4	117	7	S24209	Ig kappa chain V reg	2.53e-02
40	64	91.4	122	7	A29380	Ig kappa chain V reg	2.53e-02
41	64	91.4	123	7	S40331	Ig kappa chain - hum	2.53e-02
42	64	91.4	126	7	A34904	Ig kappa chain precu	2.53e-02
43	63	90.0	108	2	K1HUOU	Ig kappa chain V-I r	4.09e-02
44	62	88.6	98	7	PH1062	Ig light chain V reg	6.60e-02
45	62	88.6	109	7	S31998	Ig kappa chain - hum	6.60e-02

```
                                 ALIGNMENTS

RESULT     1
ENTRY        PH0087      #type fragment
TITLE        Ig kappa chain v region (anti-cyclosporin C and D) - mouse
             (fragment)
ORGANISM     #formal_name Mus musculus #common_name house mouse
DATE         15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change
             16-Aug-1996
ACCESSIONS   PH0087
REFERENCE    PH0087
             Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher,
             H.P.; Quesniaux, V.F.J.; Van Regenmortel, M.H.V.
   #journal  Mol. Immunol. (1990) 27:1029-1038
   #title    Analysis of the structural diversity of monoclonal antibodies
             to cyclosporine.
   #cross-references MUID:91042849
   #accession PH0087
   ##molecule_type mRNA
   ##residues 1-105 ##label SCH
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
FEATURE
    24-34      #region complementarity-determining 1\
    50-56      #region complementarity-determining 2\
    89-97      #region complementarity-determining 3
SUMMARY      #length 105  #checksum 9783

Query Match              97.1%;  Score 68;  DB 7;  Length 105;
Best Local Similarity    90.9%;  Pred. No. 3.54e-03;
Matches    10;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Db         24 rasqdistyln 34
              ||||||::|||
Qy          1 RASQDISSYLN 11

RESULT     2
ENTRY        S38564      #type fragment
TITLE        Ig light chain v region (ASWU1) - mouse (fragment)
ORGANISM     #formal_name Mus musculus #common_name house mouse
DATE         06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
             09-May-1997
ACCESSIONS   S38564
REFERENCE    S38559
   #authors  Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
```

```
#submission     submitted to the EMBL Data Library, September 1993
#description    Molecular analysis of mercury-induced anti-nucleolar
                antibodies in H-2s Mice.
#accession      S38564
##status        preliminary
##molecule_type mRNA
##residues      1-93 ##label MON
##cross-references EMBL:X75105
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        immunoglobulin
SUMMARY         #length 93 #checksum 1511

Query Match             95.7%;  Score 67;  DB 7;  Length 93;
Best Local Similarity   90.9%;  Pred. No. 5.82e-03;
Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db         24 rasqdisnyln 34
              |||||||:|||
Qy          1 RASQDISSYLN 11

RESULT 3
ENTRY           S69906    #type complete
TITLE           Ig kappa light chain (clone Kl4A1) - mouse
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
                09-May-1997
ACCESSIONS      S69906
REFERENCE       S69900
    #authors    Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambler, J.C.
    #journal    Immunology (1992) 75:116-121
    #title      B-cell proliferation initiated by Ia cross-linking and
                sustained by interleukins leads to class switching but not
                somatic mutation in vitro.
    #accession  S69906
    ##status    preliminary; translation not shown
    ##molecule_type DNA
    ##residues  1-107 ##label WYS
    ##cross-references EMBL:X55047
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY         #length 107 #molecular-weight 11827 #checksum 7550

Query Match             95.7%;  Score 67;  DB 7;  Length 107;
Best Local Similarity   90.9%;  Pred. No. 5.82e-03;
Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db         24 rasqdisnyln 34
              |||||||:|||
Qy          1 RASQDISSYLN 11

RESULT 4
ENTRY           B28044    #type complete
TITLE           Ig kappa chain V region (GP1) - mouse
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            19-May-1989 #sequence_revision 19-May-1989 #text_change
                16-Aug-1996
ACCESSIONS      B28044
REFERENCE       A94179
    #authors    Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
    #journal    Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
    #title      Identity of the v-kappa-10-Ars-A gene segments of the A/J and
                BALB/C strains.
    #cross-references MUID:87317629
    #accession  B28044
    ##molecule_type mRNA
    ##residues  1-107 ##label MEE
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        heterotetramer; immunoglobulin
SUMMARY         #length 107 #molecular-weight 11738 #checksum 7011

Query Match             95.7%;  Score 67;  DB 7;  Length 107;
Best Local Similarity   90.9%;  Pred. No. 5.82e-03;
```

```
Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db         24 rasqdisnyln 34
              |||||||:|||
Qy          1 RASQDISSYLN 11

RESULT 5
ENTRY           B49026    #type complete
TITLE           Ig kappa chain v region, anti-idiotypic monoclonal antibody -
                mouse
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
                25-Oct-1996
ACCESSIONS      B49026; PL0220
REFERENCE       A49026
    #authors    Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.;
                Schwartz, R.S.
    #journal    Eur. J. Immunol. (1991) 21:2185-2193
    #title      Molecular heterogeneity of auto-anti-idiotypic antibodies in
                MLR-lpr/lpr mice.
    #cross-references MUID:91364791
    #accession  B49026
    ##status    preliminary; not compared with conceptual translation
    ##molecule_type nucleic acid
    ##residues  1-107 ##label KOI
    ##cross-references NCBIP:60076
    ##experimental_source MLR-lpr/lpr
    #note       sequence extracted from NCBI backbone
REFERENCE       PL0220
    #authors    Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz,
                J.; Barrett, K.J.; Schwartz, R.S.
    #journal    J. Exp. Med. (1990) 171:1919-1930
    #title      An immunoglobulin light chain from a lupus-prone mouse
                induces autoantibodies in normal mice.
    #cross-references MUID:90278348
    #accession  PL0220
    ##status    nucleic acid sequence not shown
    ##molecule_type mRNA
    ##residues  1-107 ##label PUC
    ##experimental_source strain lupus-prone MRL-lpr/lpr mouse
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        heterotetramer; immunoglobulin
FEATURE
    24-34       #region complementarity-determining 1\
    50-56       #region complementarity-determining 2\
    89-97       #region complementarity-determining 3
SUMMARY         #length 107 #molecular-weight 11859 #checksum 8401

Query Match             95.7%;  Score 67;  DB 7;  Length 107;
Best Local Similarity   90.9%;  Pred. No. 5.82e-03;
Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db         24 rasqdisnyln 34
              |||||||:|||
Qy          1 RASQDISSYLN 11

RESULT 6
ENTRY           A28044    #type complete
TITLE           Ig kappa chain V region (22B5) - mouse
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            19-May-1989 #sequence_revision 19-May-1989 #text_change
                16-Aug-1996
ACCESSIONS      A28044
REFERENCE       A94179
    #authors    Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
    #journal    Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
    #title      Identity of the v-kappa-10-Ars-A gene segments of the A/J and
                BALB/C strains.
    #cross-references MUID:87317629
    #accession  A28044
    ##molecule_type mRNA

Query Match             95.7%;  Score 67;  DB 7;  Length 107;
Best Local Similarity   90.9%;  Pred. No. 5.82e-03;
Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db         24 rasqdisnyln 34
              |||||||:|||
Qy          1 RASQDISSYLN 11
```

```
                     ##residues        1-107 ##label MEE
CLASSIFICATION       #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS             heterotetramer; immunoglobulin
SUMMARY              #length 107  #molecular-weight 11832  #checksum 7241
Query Match          95.7%;    Score 67;   DB 7;   Length 107;
Best Local Similarity 90.9%;   Pred. No. 5.82e-03;
Matches  10;   Conservative  1;   Mismatches  0;   Indels  0;   Gaps  0;

Db    24 rasqdisnyln 34
         |||||||:|||
Qy     1 RASQDISSYLN 11

RESULT  7
ENTRY                D48677       #type fragment
TITLE                Ig light chain v-J region (24) - mouse (fragment)
ORGANISM             #formal_name Mus musculus #common_name house mouse
DATE                 19-May-1994 #sequence_revision 19-May-1994 #text_change
                     16-Aug-1996
ACCESSIONS           D48677
REFERENCE            A48677
#authors             Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
                     P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
#journal             Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
#title               Molecular characterization of monoclonal CRI-A-positive
                     anti-arsonate antibodies derived from idiotype-negative
                     mice bearing a light chain polymorphism.
#accession           D48677
##status             preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues           1-107 ##label TAS
CLASSIFICATION       #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS             immunoglobulin
SUMMARY              #length 107  #checksum 7155
Query Match          95.7%;    Score 67;   DB 7;   Length 107;
Best Local Similarity 90.9%;   Pred. No. 5.82e-03;
Matches  10;   Conservative  1;   Mismatches  0;   Indels  0;   Gaps  0;

Db    24 rasqdisnyln 34
         |||||||:|||
Qy     1 RASQDISSYLN 11

RESULT  8
ENTRY                S69901       #type complete
TITLE                Ig kappa light chain (clone KL2.21) - mouse
ORGANISM             #formal_name Mus musculus #common_name house mouse
DATE                 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
                     09-May-1997
ACCESSIONS           S69901
REFERENCE            S69900
#authors             Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal             Immunology (1992) 75:116-121
#title               B-cell proliferation initiated by Ia cross-linking and
                     sustained by interleukins leads to class switching but not
                     somatic mutation in vitro.
#accession           S69901
##status             preliminary; translation not shown
##molecule_type DNA
##residues           1-107 ##label WYS
##cross-references EMBL:X55042
CLASSIFICATION       #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY              #length 107  #molecular-weight 11857  #checksum 7740
Query Match          95.7%;    Score 67;   DB 7;   Length 107;
Best Local Similarity 90.9%;   Pred. No. 5.82e-03;
Matches  10;   Conservative  1;   Mismatches  0;   Indels  0;   Gaps  0;

Db    24 rasqdisnyln 34
         |||||||:|||
Qy     1 RASQDISSYLN 11
```

```
RESULT  9
ENTRY                S38862       #type complete
TITLE                Ig kappa chain V region - mouse
ORGANISM             #formal_name Mus musculus #common_name house mouse
DATE                 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
                     16-Aug-1996
ACCESSIONS           S38862
REFERENCE            S37200
#authors             Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.;
                     Kreuzaler, F.
#submission          submitted to the EMBL Data Library, August 1993
#description         Production and cloning of TMV-specific monoclonal antibodies.
#accession           S38862
##status             preliminary
##molecule_type mRNA
##residues           1-108 ##label FIS
##cross-references EMBL:X75854
CLASSIFICATION       #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS             heterotetramer; immunoglobulin
SUMMARY              #length 108  #molecular-weight 11865  #checksum 1422
Query Match          95.7%;    Score 67;   DB 7;   Length 108;
Best Local Similarity 90.9%;   Pred. No. 5.82e-03;
Matches  10;   Conservative  1;   Mismatches  0;   Indels  0;   Gaps  0;

Db    24 rasqdisnyln 34
         |||||||:|||
Qy     1 RASQDISSYLN 11

RESULT  10
ENTRY                S69903       #type complete
TITLE                Ig kappa light chain (clone KL2.29) - mouse
ORGANISM             #formal_name Mus musculus #common_name house mouse
DATE                 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
                     09-May-1997
ACCESSIONS           S69903
REFERENCE            S69900
#authors             Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal             Immunology (1992) 75:116-121
#title               B-cell proliferation initiated by Ia cross-linking and
                     sustained by interleukins leads to class switching but not
                     somatic mutation in vitro.
#accession           S69903
##status             preliminary; translation not shown
##molecule_type DNA
##residues           1-108 ##label WYS
##cross-references EMBL:X55044
CLASSIFICATION       #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY              #length 108  #molecular-weight 11931  #checksum 1846
Query Match          95.7%;    Score 67;   DB 7;   Length 108;
Best Local Similarity 90.9%;   Pred. No. 5.82e-03;
Matches  10;   Conservative  1;   Mismatches  0;   Indels  0;   Gaps  0;

Db    24 rasqdisnyln 34
         |||||||:|||
Qy     1 RASQDISSYLN 11

RESULT  11
ENTRY                S69902       #type complete
TITLE                Ig kappa light chain (clone KL2.28) - mouse
ORGANISM             #formal_name Mus musculus #common_name house mouse
DATE                 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
                     09-May-1997
ACCESSIONS           S69902
REFERENCE            S69900
#authors             Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal             Immunology (1992) 75:116-121
#title               B-cell proliferation initiated by Ia cross-linking and
```

```
                    sustained by interleukins leads to class switching but not
                    somatic mutation in vitro.
#accession          S69902
##status            preliminary; translation not shown
##molecule_type     DNA
##residues          1-108 ##label WYS
##cross-references  EMBL:X55043
CLASSIFICATION      #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY             #length 108 #molecular-weight 11895 #checksum 1228

Query Match            95.7%;   Score 67;   DB 7;   Length 108;
Best Local Similarity  90.9%;   Pred. No. 5.82e-03;
Matches   10;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

Db    24  rasqdisnyln 34
          |||||||:|||
Qy     1  RASQDISSYLN 11


RESULT  12
ENTRY          S69900        #type complete
TITLE          Ig kappa light chain (clone KL2.18) - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
               09-May-1997
ACCESSIONS     S69900
REFERENCE      S69900
#authors       Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal       Immunology (1992) 75:116-121
#title         B-cell proliferation initiated by Ia cross-linking and
               sustained by interleukins leads to class switching but not
               somatic mutation in vitro.
#accession     S69900
##status       preliminary; translation not shown
##molecule_type DNA
##residues     1-108 ##label WYS
##cross-references EMBL:X55041
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY        #length 108 #molecular-weight 11954 #checksum 1768

Query Match            95.7%;   Score 67;   DB 7;   Length 108;
Best Local Similarity  90.9%;   Pred. No. 5.82e-03;
Matches   10;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

Db    24  rasqdisnyln 34
          |||||||:|||
Qy     1  RASQDISSYLN 11


RESULT  13
ENTRY          KVMSAR        #type complete
TITLE          Ig kappa chain v regions (anti-arsonate hybridoma proteins) -
               mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change
               16-Aug-1996
ACCESSIONS     A01927
REFERENCE      A01927
#authors       Siegelman, M.; Capra, J.D.
#journal       Proc. Natl. Acad. Sci. U.S.A. (1981) 78:7679-7683
#title         Complete amino acid sequence of light chain variable regions
               derived from five monoclonal anti-p-azophenylarsonate
               antibodies differing with respect to a crossreactive
               idiotype.
#cross-references MUID:82150934
#accession     A01927
##molecule_type protein
##residues     1-108 ##label SIE
##experimental_source strain A/J
##note         hP 93G7 differs in having 93-Met; HP 123E6 differs in
               having 7-Ser, 92-Tyr, and 93-Met; HP 124E1 differs in
               having 30-Asn, 92-Lys, and 93-Thr; and HP 91A3 differs
               in having 8-Pro, 30-Asn, 37-Arg, 84-Ser, and 93-Ala
```

```
COMMENT        The sequence shown is HP R16.7.
COMPLEX        An immunoglobulin heterotetramer subunit consists of two
               identical light (kappa or lambda) and two identical heavy
               (alpha, delta, epsilon, gamma, or mu) chains usually
               stabilized by interchain disulfide bonds. In some cases,
               such as IgA and IgM, the subunits associate into larger
               oligomers.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer
FEATURE
   23-88       #disulfide_bonds #status predicted
SUMMARY        #length 108 #molecular-weight 11910 #checksum 1537

Query Match            95.7%;   Score 67;   DB 2;   Length 108;
Best Local Similarity  90.9%;   Pred. No. 5.82e-03;
Matches   10;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

Db    24  rasqdisnyln 34
          |||||||:|||
Qy     1  RASQDISSYLN 11


RESULT  14
ENTRY          C26405        #type complete
TITLE          Ig kappa chain v region (3D10) - mouse
ORGANISM       #forma_name Mus musculus #common_name house mouse
DATE           30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
               16-Aug-1996
ACCESSIONS     C26405
REFERENCE      A90518
#authors       Smith, J.A.; Margolies, M.N.
#journal       Biochemistry (1987) 26:604-612
#title         Complete amino acid sequences of the heavy and light chain
               variable regions from two A/J mouse antigen nonbinding
               monoclonal antibodies bearing the predominant p-azophenyl
               arsonate idiotype.
#cross-references MUID:87157677
#accession     C26405
##molecule_type protein
##residues     1-108 ##label SMI
##experimental_source strain A/J
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 108 #molecular-weight 11944 #checksum 1684

Query Match            95.7%;   Score 67;   DB 7;   Length 108;
Best Local Similarity  90.9%;   Pred. No. 5.82e-03;
Matches   10;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

Db    24  rasqdisnyln 34
          |||||||:|||
Qy     1  RASQDISSYLN 11


RESULT  15
ENTRY          PL0282        #type fragment
TITLE          Ig light chain v region (45-49, anti p-azophenylarsonate) -
               mouse (fragment)
ORGANISM       #forma_name Mus musculus #common_name house mouse
DATE           24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change
               16-Aug-1996
ACCESSIONS     PL0282
REFERENCE      PL0281
#authors       Wysocki, L.J.; Gefter, M.L.; Margolies, M.N.
#journal       J. Exp. Med. (1990) 172:315-323
#title         Parallel evolution of antibody variable regions by somatic
               processes: Consecutive shared somatic alterations in VH
               genes expressed by independently generated hybridomas
               apparently acquired by point mutation and selection rather
               than by gene conversion.
#accession     PL0282
##molecule_type mRNA
##residues     1-108 ##label WYS
```

```
        ##experimental_source A/J mice
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS        immunoglobulin
SUMMARY         #length 108 #checksum 960

Query Match           95.7%;   Score 67;  DB 7; Length 108;
Best Local Similarity 90.9%;   Pred. No. 5.82e-03;
Matches  10; Conservative   1; Mismatches  0;  Indels   0;  Gaps   0;

Db   24 rasqdisnyln 34
        |||||||:|||
Qy    1 RASQDISSYLN 11

Search completed: Tue Mar  3 11:19:18 1998
Job time : 11 secs.
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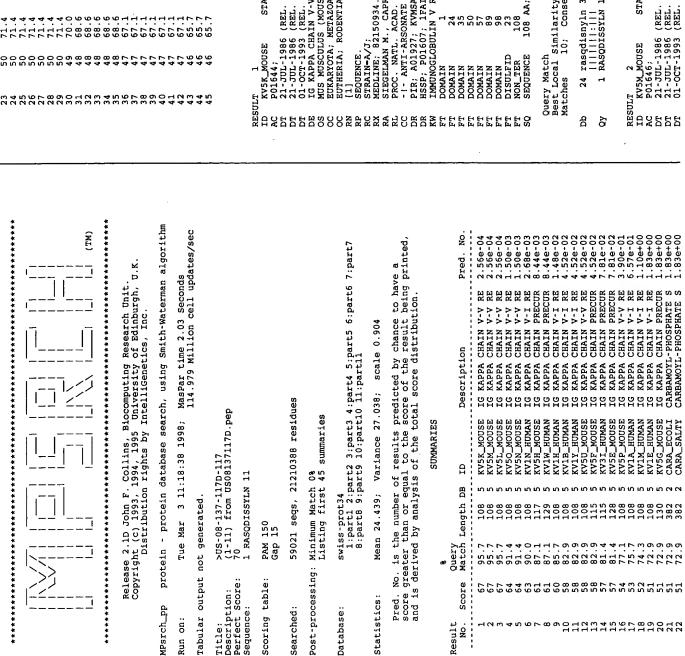
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```
  M M         M M     PP     SS     RR     CC     H   H
  MM MM      MM MM   P  P   S       R  R   C      H   H
  M M M     M M M    PP     SS      RR     C      HHHHH
  M   M    M   M     P        SS    R R    C      H   H
  M   M   M   M      P      SSSS    R  R    CC    H   H   (TM)
```

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 3 11:18:38 1998;   MasPar time 2.03 Seconds
               114.979 Million cell updates/sec
Tabular output not generated.

Title: >US-08-137-117D-117
Description: (1-11) from US08137117D.pep
Perfect Score: 70
Sequence: 1 RASQDISSYLN 11

Scoring table: PAM 150
                Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: swiss-prot34
                1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                8:part8 9:part9 10:part10 11:part11

Statistics: Mean 24.439; Variance 27.038; scale 0.904

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                SUMMARIES

                %
Result   Query
No.   Score Match Length DB ID   Description   Pred. No.
---- ----- ----- ------ -- --   -----------   --------
  1   67   95.7   108   5 KV5K_MOUSE   IG KAPPA CHAIN V-V RE   2.56e-04
  2   67   95.7   108   5 KV5M_MOUSE   IG KAPPA CHAIN V-V RE   2.56e-04
  3   67   95.7   108   5 KV5L_MOUSE   IG KAPPA CHAIN V-V RE   2.56e-04
  4   64   91.4   108   5 KV5O_MOUSE   IG KAPPA CHAIN V-V RE   1.50e-03
  5   64   91.4   108   5 KV5N_MOUSE   IG KAPPA CHAIN V-V RE   1.50e-03
  6   63   90.0   117   5 KV1N_HUMAN   IG KAPPA CHAIN V-I RE   2.68e-03
  7   61   87.1   108   5 KV5P_MOUSE   IG KAPPA CHAIN PRECUR   8.44e-03
  8   61   87.1   129   5 KV1W_HUMAN   IG KAPPA CHAIN PRECUR   8.44e-03
  9   60   85.7   108   5 KV1H_HUMAN   IG KAPPA CHAIN V-I RE   1.48e-02
 10   58   82.9   108   5 KV1Y_HUMAN   IG KAPPA CHAIN V-I RE   4.52e-02
 11   58   82.9   108   5 KV5U_MOUSE   IG KAPPA CHAIN V-V RE   4.52e-02
 12   58   82.9   115   5 KV5F_MOUSE   IG KAPPA CHAIN PRECUR   4.52e-02
 13   57   81.4   115   5 KV3I_HUMAN   IG KAPPA CHAIN PRECUR   7.81e-02
 14   57   81.4   128   5 KV5E_MOUSE   IG KAPPA CHAIN PRECUR   7.81e-02
 15   54   77.1   108   5 KV5P_MOUSE   IG KAPPA CHAIN V-V RE   3.90e-01
 16   53   75.7   108   5 KV1A_HUMAN   IG KAPPA CHAIN V-I RE   6.57e-01
 17   52   74.3   108   5 KV1M_HUMAN   IG KAPPA CHAIN V-I RE   1.10e+00
 18   51   72.9   108   5 KV1E_HUMAN   IG KAPPA CHAIN V-I RE   1.83e+00
 19   51   72.9   130   5 KV5G_MOUSE   IG KAPPA CHAIN PRECUR   1.83e+00
 20   51   72.9   382   2 CARA_ECOLI   CARBAMOYL-PHOSPHATE S   1.83e+00
 21   51   72.9   382   2 CARA_SALTY   CARBAMOYL-PHOSPHATE S   1.83e+00
 22   50   71.4   107   5 KV1D_HUMAN   IG KAPPA CHAIN V-I RE   3.02e+00
 23   50   71.4   108   5 KV5D_MOUSE   IG KAPPA CHAIN V-V RE   3.02e+00
 24   50   71.4   108   5 KV1P_HUMAN   IG KAPPA CHAIN V-I RE   3.02e+00
 25   50   71.4   108   5 KV07_RABIT   IG KAPPA CHAIN V REGI   3.02e+00
 26   50   71.4   108   5 KV1O_HUMAN   IG KAPPA CHAIN V-I RE   3.02e+00
 27   50   71.4   117   3 KV10_RABIT   IG KAPPA CHAIN V REGI   3.02e+00
 28   50   71.4   1342   3 ERB3_HUMAN   ERBB-3 RECEPTOR PROTE   3.02e+00
 29   49   70.0   108   5 KV5J_MOUSE   IG KAPPA CHAIN V-V RE   4.95e+00
 30   48   68.6   133   8 PSSR_ECOLI   POSSIBLE REGULATORY P   8.04e+00
 31   48   68.6   199   7 PRL_BALBO   PROLACTIN (PRL).   8.04e+00
 32   48   68.6   199   7 PRL_LOXAF   PROLACTIN (PRL).   8.04e+00
 33   48   68.6   229   7 PRL_FELCA   PROLACTIN PRECURSOR (8.04e+00
 34   47   67.1   312   6 NIFU_AZOVI   NIFU PROTEIN.   1.30e+01
 35   47   67.1   108   5 KV1S_HUMAN   IG KAPPA CHAIN V-I RE   1.30e+01
 36   47   67.1   117   5 KV1J_HUMAN   IG KAPPA CHAIN PRECUR   1.30e+01
 37   47   67.1   129   5 KV1X_HUMAN   IG KAPPA CHAIN PRECUR   1.30e+01
 38   47   67.1   199 11 YAJG_HAEIN   HYPOTHETICAL LIPOPROT   1.30e+01
 39   47   67.1   235 11 YIQ1_YEAST   HYPOTHETICAL 27.1 KD   1.30e+01
 40   47   67.1   274   9 T2E1_HERAU   TYPE II RESTRICTION E   1.30e+01
 41   47   67.1   943   5 IROA_NEIME   IRON-REGULATED OUTER   1.30e+01
 42   46   65.7   451   7 PHOQ_SALTY   VIRULENCE SENSOR PROT   2.07e+01
 43   46   65.7   1132 10 VHSJ_LAMBD   HOST SPECIFICITY PROT   2.07e+01
 44   46   65.7   1507 11 YY06_HUMAN   HYPOTHETICAL MYELOID   2.07e+01
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ALIGNMENTS

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RESULT   1
ID   KV5K_MOUSE     STANDARD;      PRT;    108 AA.
AC   P01644;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP R16.7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN          1     23       FRAMEWORK 1.
FT   DOMAIN         24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN         35     49       FRAMEWORK 2.
FT   DOMAIN         50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN         57     88       FRAMEWORK 3.
FT   DOMAIN         89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN         98    108       FRAMEWORK 4.
FT   DISULFID       23     88       BY SIMILARITY.
FT   NON_TER       108    108
SQ   SEQUENCE      108 AA;     11910 MW;     64A62905 CRC32;

     Query Match          95.7%;       Score 67;  DB 5;  Length 108;
     Best Local Similarity 90.9%;       Pred. No. 2.56e-04;
     Matches    10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db      24 rasqdisnyln 34
           ||||||:|||
Qy       1 RASQDISSYLN 11

RESULT   2
ID   KV5M_MOUSE     STANDARD;      PRT;    108 AA.
AC   P01646;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
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DE   IG KAPPA CHAIN V-V REGION (HP 123E6).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN          1      23    FRAMEWORK 1.
FT   DOMAIN         24      34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN         35      49    FRAMEWORK 2.
FT   DOMAIN         50      56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN         57      88    FRAMEWORK 3.
FT   DOMAIN         89      97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN         98     108    FRAMEWORK 4.
FT   DISULFID       23      88    BY SIMILARITY.
FT   NON_TER       108     108
SQ   SEQUENCE      108 AA;  11989 MW;  23B8B67 CRC32;

Query Match              95.7%;  DB 5;  Length 108;
Best Local Similarity    90.9%;  Pred. No. 2.56e-04;  Indels 0;  Gaps 0;
Matches    10;  Conservative    0;  Mismatches    1;

Db        24 rasqdisnyln 34
             |||||||:|||
Qy         1 RASQDISSYLN 11


RESULT   3
ID   KV5L_MOUSE      STANDARD;       PRT;   108 AA.
AC   P01645;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 93G7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN          1      23    FRAMEWORK 1.
FT   DOMAIN         24      34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN         35      49    FRAMEWORK 2.
FT   DOMAIN         50      56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN         57      88    FRAMEWORK 3.
FT   DOMAIN         89      97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN         98     108    FRAMEWORK 4.
FT   DISULFID       23      88    BY SIMILARITY.
FT   NON_TER       108     108
SQ   SEQUENCE      108 AA;  11954 MW;  A203E130 CRC32;

Query Match              95.7%;  DB 5;  Length 108;
Best Local Similarity    90.9%;  Pred. No. 2.56e-04;  Indels 0;  Gaps 0;
Matches    10;  Conservative    0;  Mismatches    1;

Db        24 rasqdisnyln 34
             |||||||:|||
Qy         1 RASQDISSYLN 11


RESULT   4
ID   KV5O_MOUSE      STANDARD;       PRT;   108 AA.
AC   P01648;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 91A3).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN          1      23    FRAMEWORK 1.
FT   DOMAIN         24      34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN         35      49    FRAMEWORK 2.
FT   DOMAIN         50      56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN         57      88    FRAMEWORK 3.
FT   DOMAIN         89      97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN         98     108    FRAMEWORK 4.
FT   DISULFID       23      88    BY SIMILARITY.
FT   NON_TER       108     108
SQ   SEQUENCE      108 AA;  11961 MW;  5B067780 CRC32;

Query Match              91.4%;  Score 64;  DB 5;  Length 108;
Best Local Similarity    81.8%;  Pred. No. 1.50e-03;  Indels 0;  Gaps 0;
Matches     9;  Conservative    2;  Mismatches    2;

Db        24 rasqdinnyln 34
             |||||||::|||
Qy         1 RASQDISSYLN 11


RESULT   5
ID   KV5N_MOUSE      STANDARD;       PRT;   108 AA.
AC   P01647;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 124E1).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN          1      23    FRAMEWORK 1.
FT   DOMAIN         24      34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN         35      49    FRAMEWORK 2.
FT   DOMAIN         50      56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN         57      88    FRAMEWORK 3.
FT   DOMAIN         89      97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN         98     108    FRAMEWORK 4.
FT   DISULFID       23      88    BY SIMILARITY.
FT   NON_TER       108     108
SQ   SEQUENCE      108 AA;  11965 MW;  84754175 CRC32;

Query Match              91.4%;  Score 64;  DB 5;  Length 108;
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Best Local Similarity 81.8%;   Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Matches   9;

Db   24 rasqdinnyln 34
          |||||::|||
Qy   1 RASQDISSYLN 11

RESULT 6
ID   KV1N_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01606;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (OU).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 70201507.
RA   KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
RL   SCIENCE 169:56-59(1970).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR   PIR; A01872; K1HUOU.
     HSSP; P01607; 2FGW.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11777 MW; 4B089785 CRC32;

Query Match 90.0%;   DB 5; Length 108;
Best Local Similarity 72.7%; Pred. No. 2.68e-03;
Matches   8;   Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db   24 rasztissylb 34
          |||||:||::|
Qy   1 RASQDISSYLN 11

RESULT 7
ID   KV5H_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01641;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81064681.
RA   MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;
RL   CELL 21:793-799(1980).
DR   EMBL; K00880; G197444; -.
DR   PIR; A01924; KVMS3B.
     HSSP; P01607; 1FGV.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL   1   22
FT   CHAIN   23   117   IG KAPPA CHAIN V-V REGION (MOPC 173B).
FT   DOMAIN   23   45   FRAMEWORK 1.
FT   DOMAIN   46   56   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   57   71   FRAMEWORK 2.
FT   DOMAIN   72   78   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   79   110   FRAMEWORK 3.
FT   DOMAIN   111   >117   COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID   45   110   BY SIMILARITY.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 12954 MW; 38F2B08C CRC32;

Query Match 87.1%;   DB 5; Length 117;
Best Local Similarity 81.8%; Pred. No. 8.44e-03;
Matches   9;   Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Db   46 rasqdihgyln 56
          ||||| :||
Qy   1 RASQDISSYLN 11

RESULT 8
ID   KV1W_HUMAN   STANDARD;   PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85014148.
RA   KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
RL   NUCLEIC ACIDS RES. 12:6995-7005(1984).
DR   EMBL; X00965; G296684; ALT_TERM.
DR   PIR; A01883; K1HVWK.
     HSSP; P01607; 2FGW.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL   1   22
FT   CHAIN   23   129   IG KAPPA CHAIN V-I REGION (WALKER).
FT   DOMAIN   23   45   FRAMEWORK 1.
FT   DOMAIN   46   56   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   57   71   FRAMEWORK 2.
FT   DOMAIN   72   78   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   79   110   FRAMEWORK 3.
FT   DOMAIN   111   119   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   120   129   FRAMEWORK 4.
FT   DISULFID   45   110   BY SIMILARITY.
FT   NON_TER   129   129
SQ   SEQUENCE   129 AA; 14069 MW; 99925172 CRC32;

Query Match 87.1%;   DB 5; Length 129;
Best Local Similarity 81.8%; Pred. No. 8.44e-03;
Matches   9;   Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Db   46 rasqsisnyln 56
          ||||| ||:|||
Qy   1 RASQDISSYLN 11

RESULT 9
ID   KV1H_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (HAU).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 71032830.
RA   WATANABE S., HILSCHMANN N.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1291-1295(1970).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS IS A BENCE-JONES PROTEIN.

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DR   PIR; A01868; KIHUHU.
DR   HSSP; P01607; 1FVC.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;    11671 MW;   C8A2EE86 CRC32;

Query Match             85.7%;  Score 60;  DB 5;  Length 108;
Best Local Similarity   81.8%;  Pred. No. 1.48e-02;
Matches    9;  Conservative    9;  Mismatches    1;  Indels    0;  Gaps    0;

Db         24  rasqsissyls 34
               |||| |||||:
Qy          1  RASQDISSYLN 11

RESULT    10
ID   KV1B_HUMAN     STANDARD;      PRT;     108 AA.
AC   P01594;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (AU).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 72189444.
RA   SCHIECHL H., HILSCHMANN N.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE; 77022433.
RA   FEHLHAMMER H., SCHIFFER M., EPP O., COLMAN P.M., LATTMAN E.E.,
RA   SCHWAGER P., STEIGEMANN W., SCHRAMM H.J.;
RL   BIOPHYS. STRUCT. MECH. 1:139-146(1975).
CC   -!- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR
CC       REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF
CC       THE KAPPA CHAIN REI.
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; KIHUAU.
DR   HSSP; P01607; 1IGM.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;    11939 MW;   B455AF00 CRC32;

Query Match             82.9%;  Score 58;  DB 5;  Length 108;
Best Local Similarity   81.8%;  Pred. No. 4.52e-02;
Matches    9;  Conservative    9;  Mismatches    1;  Indels    0;  Gaps    0;

Db         24  qasqdisdyln 34
               :||||| ||
Qy          1  RASQDISSYLN 11

RESULT    11
ID   KV1Y_HUMAN     STANDARD;      PRT;     108 AA.
AC   P80362;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (WAT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE; 95086080.
RA   HUANG D.-B., CHANG C.-H., AINSWORTH C., BRUENGER A.T., EULITZ M.,
RA   SOLOMON A., STEVENS F.J., SCHIFFER M.;
RL   BIOCHEMISTRY 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE; 81267384.
RA   STEVENS F.J., WESTHOLM F.A., PANAGIOTOPOULOS N., SCHIFFER M.,
RA   POPP R.A., SOLOMON A.;
RL   J. MOL. BIOL. 147:185-193(1981).
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   CONFLICT     30     31       TN -> SD (IN REF. 2).
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;    11737 MW;   41A2388C CRC32;

Query Match             82.9%;  Score 58;  DB 5;  Length 108;
Best Local Similarity   72.7%;  Pred. No. 4.52e-02;
Matches    8;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Db         24  rasqditnyvn 34
               |||||::|:|
Qy          1  RASQDISSYLN 11

RESULT    12
ID   KV5U_MOUSE     STANDARD;      PRT;     108 AA.
AC   P04946;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (NQ5-89.4).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83271467.
RA   KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
RL   NATURE 304:320-324(1983).
CC   -!- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
DR   EMBL; K00745; G196455; -.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
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SQ   SEQUENCE   108 AA;  11866 MW;  D396F142 CRC32;

     Query Match                              Score  58;  DB 5;  Length 108;
     Best Local Similarity  82.9%;  90.0%;    Pred. No. 4.52e-02;
     Matches   9;  Conservative  8;  Mismatches  1;  Indels  0;  Gaps  0;

Db   25  asqdisnyln  34
         ||||||:|||
Qy    2  ASQDISSYLN  11

RESULT 13
ID   KV5F_MOUSE     STANDARD;      PRT;   115 AA.
AC   P01638;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (L6) (FRAGMENT).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81220975.
RA   PECH M., HOCHTL J., SCHNELL H., ZACHAU H.G.;
RL   NATURE 291:668-670(1981).
DR   PIR; A01921; KVMSL6.
DR   HSSP; P01607; 1IIF.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21   >115       IG KAPPA CHAIN V-V REGION (L6).
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       77    108       FRAMEWORK 3.
FT   DOMAIN      109   >115       COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12986 MW;  958689AF CRC32;

     Query Match                              Score  58;  DB 5;  Length 115;
     Best Local Similarity  82.9%;  72.7%;    Pred. No. 4.52e-02;
     Matches   8;  Conservative  8;  Mismatches  3;  Indels  0;  Gaps  0;

Db   44  kasqdinsyls  54
         :||||||:|||:
Qy    1  RASQDISSYLN  11

RESULT 14
ID   KV3I_HUMAN     STANDARD;      PRT;   115 AA.
AC   P04433;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85087932.
RA   PECH M., ZACHAU H.G.;
RL   NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR   EMBL; X01668; -.; NOT_ANNOTATED_CDS.
DR   PIR; A01900; K3HUVG.
DR   HSSP; P01607; 1AAG.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21   >115       IG KAPPA CHAIN V-III REGION (VG).
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       77    108       FRAMEWORK 3.
FT   DISULFID     43    108       COMPLEMENTARITY-DETERMINING 3.
FT   NON_TER     115    115       BY SIMILARITY.
SQ   SEQUENCE   115 AA;  12575 MW;  37E182FC CRC32;

     Query Match                              Score  57;  DB 5;  Length 115;
     Best Local Similarity  81.4%;  80.0%;    Pred. No. 7.81e-02;
     Matches   8;  Conservative  1;  Mismatches  1;  Indels  1;  Gaps  0;

Db   44  rasqsvssyl  53
         |||| :||||
Qy    1  RASQDISSYL  10

RESULT 15
ID   KV5E_MOUSE     STANDARD;      PRT;   128 AA.
AC   P01637;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (T1).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81052342.
RA   ALTENBURGER W., STEINMETZ M., ZACHAU H.G.;
RL   NATURE 287:603-607(1980).
DR   EMBL; V00772; G762979; -.
DR   PIR; A01920; KVMST1.
DR   HSSP; P01607; 1IIF.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL        1     20
FT   CHAIN        21    128       IG KAPPA CHAIN V-V REGION (T1).
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       77    108       FRAMEWORK 3.
FT   DOMAIN      109    117       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      118    127       FRAMEWORK 4.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     128    128
SQ   SEQUENCE   128 AA;  14385 MW;  87009E44 CRC32;

     Query Match                              Score  57;  DB 5;  Length 128;
     Best Local Similarity  81.4%;  80.0%;    Pred. No. 7.81e-02;
     Matches   8;  Conservative  2;  Mismatches  2;  Indels  0;  Gaps  0;

Db   44  kasqdinsyl  53
         :||||||:||
Qy    1  RASQDISSYL  10

Search completed: Tue Mar  3 11:18:47 1998
Job time : 9 secs.
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| | \ / | ||  __/   ___) | |  _ < | |___  |  _  |
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar   3 14:28:08 1998; MasPar time 8.47 Seconds
                                           11.473 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117D-118
Description: (1-7) from US08137117D.pep
Perfect Score: 51
Sequence: 1 YTSRLHS 7

Scoring table: PAM 150
               Gap 15

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a-geneseq30
               1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
               8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
               14:part14 15:part15 16:part16 17:part17 18:part18
               19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 15.572; Variance 37.258; scale 0.418

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                   SUMMARIES

                 %
Result   Query
No.   Score Match Length DB ID   Description   Pred. No.
----- ----- ----- ------ -- -------   -----------   ---------
  1   51 100.0   88 9 R47210   Chimeric human/mouse   5.83e+00
  2   51 100.0   107 6 R30768   Murine anti-CD3 MAb U   5.83e+00
  3   51 100.0   108 20 W00834   Variable light chain   5.83e+00
  4   51 100.0   108 17 W04177   Variant variable ligh   5.83e+00
  5   51 100.0   109 19 R52039   Light chain variable   5.83e+00
  6   51 100.0   124 9 R47206   Human/murine IL-1 chi   5.83e+00
  7   51 100.0   126 5 R29015   pUC-RV1-PM1a.   5.83e+00
  8   51 100.0   126 5 R29013   pUC-RVh-PM1a.   5.83e+00
  9   51 100.0   127 22 W11815   Mouse anti-human Fas   5.83e+00
 10   51 100.0   127 22 W11817   Humanised mouse anti-   5.83e+00
 11   51 100.0   127 5 R28670   ppM-k3 protein produc   5.83e+00
 12   51 100.0   127 6 R32121   Anti-CD4 antibody MT   5.83e+00
 13   51 100.0   128 19 W06215   MAb ME4 light chain v   5.83e+00
 14   51 100.0   128 5 R09426   ME4 Light Chain V Reg   5.83e+00
 15   51 100.0   129 9 R47207   Human/murine IL-1 chi   5.83e+00
 16   51 100.0   131 14 R84553   MAb SCH94.03 light ch   5.83e+00
 17   51 100.0   268 8 R44226   Chimeric Ig superfami   5.83e+00
 18   51 100.0   302 10 R60206   Bispecific CD3-L6FvIg   5.83e+00
 19   46   90.2   127 19 R99003   MAb VL1786 light chai   2.76e+01
 20   46   90.2   1422 16 R82071   Hepatitis GB virus (H   2.76e-01
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 21     42   82.4    107  6 R30769    huxCD3v9, humanised m    9.19e+01
 22     42   82.4    140  5 R27559    Cyn d allergen B1.       9.19e+01
 23     41   80.4    107 13 R77302    Variable light chain     1.23e+02
 24     41   80.4    126  2 R12237    Mouse MAb 1C11 L chai    1.23e+02
 25     41   80.4    127  2 R12359    Light (kappa) chain v    1.23e+02
 26     41   80.4    273  9 R52865    Anti-influenza N10 sc    1.23e+02
 27     41   80.4    539 21 W20778    H. pylori cytoplasmic    1.23e+02
 28     40   78.4    127  7 R39265    Mouse C4G1 Ig light-c    1.65e+02
 29     40   78.4    172 17 W00482    Human deoxycytidine k    1.65e+02
 30     40   78.4    214  6 R30776    H52L6-158 murine anti    1.65e+02
 31     40   78.4    214 19 W00373    Anti-CD18 chimeric an    1.65e+02
 32     40   78.4    214  6 R43338    Completely humanised     1.65e+02
 33     40   78.4    233  6 R30777    pH52-9.0 humanised mu    1.65e+02
 34     40   78.4    706 12 R68743    BCL-6 zinc finger pro    1.65e+02
 35     40   78.4   1235 22 W21572    Rat brain serine ecto    1.65e+02
 36     40   78.4   1249 22 W21571    Rat brain homologue o    1.65e+02
 37     39   76.5    127  5 R29010    p146-k3 protein produ    2.20e+02
 38     39   76.5    432 15 R92813    Murine interleukin-11    2.20e+02
 39     39   76.5    441 17 R99091    Murine Etl-2 gene pro    2.20e+02
 40     39   76.5    928 14 R77399    BHV1 gI glycoprotein.    2.20e+02
 41     39   76.5    933  5 R27807    Bovine herpes virus t    2.20e+02
 42     39   76.5    933  7 R41343    Bovine herpesvirus ty    2.20e+02
 43     38   74.5    745 13 R76110    Human ALD.               2.93e+02
 44     38   74.5    794 23 W25637    Human cadherin-12.       2.93e+02
 45     38   74.5    842  4 P93712    Sequence of infectiou    2.93e+02
```

                                  ALIGNMENTS

```
RESULT   1
ID   R47210 standard; protein; 88 AA.
AC   R47210;
DT   09-AUG-1994  (first entry)
DE   Chimeric human/mouse antibody L chain mature peptide.
KW   Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;
KW   light; L; chain; constant; region; variable; mouse; anti-human; PCR;
KW   graft; CDR; complementarity determining region; heavy; H; detection;
KW   inflammatory disease; arteriosclerosis; polymerase chain reaction;
KW   diffused intravascular coagulation; leukemia; amplify.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus musculus.
PN   WO9402627-A.
PD   03-FEB-1994.
PF   08-JUL-1993; J00941.
PR   16-JUL-1992; JP-189248.
PA   (SAKA ) OTSUKA PHARM CO LTD.
PI   Hirai Y, Nishida T,  Omoto Y,  Owens RJ;
DR   WPI: 94-048885/06.
DR   N-PSDB; Q56075.
PT   Mouse/human chimeric antibody against human interleukin-1 - for
PT   treatment of diseases in which production of interleukin-1 is
PT   abnormal, and for diagnostic imaging of interleukin-1 production
PT   sites in vivo
PS   Disclosure; Fig 18; 58pp; Japanese.
CC   This sequence represents the mature L chain of a chimeric recombinant
CC   antibody against human interleukin-1 (IL-1).  The chimeric antibody
CC   has a light (L) chain in which the constant region is that of a human
CC   antibody and the variable region is from a mouse anti-human IL-1
CC   antibody or is a mouse-human graft containing the CDR regions of mouse
CC   anti-human IL-1 antibody, and a heavy (H) chain in which the constant
CC   region is that of a human antibody and the variable region is from a
CC   mouse anti-human IL-1 antibody or is a mouse-human graft containing
CC   the CDR regions of mouse anti-human IL-1 antibody.  The chimeric
CC   antibody is used to treat diseases in which abnormal amounts of IL-1
CC   are produced, eg. inflammatory disease, arteriosclerosis, diffused
CC   intravascular coagulation or leukemia.  It can also be labelled and
CC   used for diagnostic imaging of IL-1 producing sites in vivo.
SQ   Sequence 88 AA;

Query Match             100.0%;  Score 51; DB 9; Length 88;
Best Local Similarity   100.0%;  Pred. No. 5.83e+00;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db   34 ytsrlhs 40
     ||||||
Qy   1 YTSRLHS 7

RESULT 2
ID R30768 standard; protein; 107 AA.
AC R30768;
DT 12-MAY-1993 (first entry)
DE Murine anti-CD3 MAb UCHT1 light chain variable domain.
KW Humanisation; rapid; monoclonal antibody; muxCD3.
OS Mus musculus.
PN WO9222653-A.
PD 23-DEC-1992.
PF 15-JUN-1992; U05126.
PR 14-JUN-1991; US-715272.
PA (GETH) GENENTECH INC.
PI Carter PJ, Presta LG.
DR WPI; 93-018139/02.
PT Humanisation of antibodies - by molecular modelling of the variable
PT domains and alteration by gene conversion mutagenesis
PS Disclosure; Fig 5; 126pp; English.
CC The sequence is that of the light chain variable domain of murine
CC anti-CD3 monoclonal antibody UCHT1 (muxCD3, Shalaby 1992).
SQ Sequence 107 AA;

Query Match   100.0%;   Score 51;   DB 6;   Length 107;
Best Local Similarity 100.0%;   Pred. No. 5.83e+00;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   50 ytsrlhs 56
     ||||||
Qy   1 YTSRLHS 7

RESULT 3
ID W00834 standard; Protein; 108 AA.
AC W00834;
DT 20-MAY-1997 (first entry)
DE Variable light chain of anti-human Fas ligand antibody NOK-1.
KW Variable region; light chain; human; Fas ligand; monoclonal;
KW antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;
KW diagnosis; disease; hepatitis; infectious mononucleosis;
OS systemic lupus erythematosus.
OS Mus musculus.
PN WO9629350-A1.
PD 26-SEP-1996.
PF 21-MAR-1996; J00734.
PR 20-MAR-1995; JP-087420.
PR 27-OCT-1995; JP-303492.
PA (SUME) SUMITOMO ELECTRIC IND CO.
PI Kayagaki N, Nakata M, Okumura K, Yagita H;
DR WPI; 96-443140/44.
DR N-PSDB; T39560.
PT Monoclonal antibody specifically recognising the Fas ligand - useful
PT for the detection of Fas ligands either on cell surface or in
PT solution
PS Claim 41; Pages 93-94; 133pp; Japanese.
CC The present sequence is the light chain variable region of the
CC anti-human Fas ligand monoclonal antibody (MAb) NOK-1. NOK-1 is
CC produced by the hybridoma NOK-1 (FERM BP-5044), which was prepared
CC by immunising mice with transformed human Fas ligand expressing COS
CC cells, and fusing spleen cells isolated from the mice with myeloma
CC P3x63Ag8.653 (ATCC CRL-1580) cells. The MAb recognises the human
CC Fas ligand on the cell surface or in solution, and can be used to
CC inhibit the apoptosis inducing cell surface Fas ligand/Fas
CC reaction. The MAb can also be used for a Fas ligand assay in
CC biological samples (e.g. human blood), especially for disease
CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
CC lupus erythematosus
SQ Sequence 108 AA;

Query Match   100.0%;   Score 51;   DB 20;   Length 108;

Best Local Similarity 100.0%;   Pred. No. 5.83e+00;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   50 ytsrlhs 56
     ||||||
Qy   1 YTSRLHS 7

RESULT 4
ID W04177 standard; Protein; 108 AA.
AC W04177;
DT 19-MAY-1997 (first entry)
DE Variant variable light chain of Fas ligand antibody NOK-1.
KW Variable region; light chain; human; Fas ligand; monoclonal;
KW antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;
KW diagnosis; disease; hepatitis; infectious mononucleosis;
KW systemic lupus erythematosus; variant.
OS Mus musculus.
PN WO9629350-A1.
PD 26-SEP-1996.
PF 21-MAR-1996; J00734.
PR 20-MAR-1995; JP-087420.
PR 27-OCT-1995; JP-303492.
PA (SUME) SUMITOMO ELECTRIC IND CO.
PI Kayagaki N, Nakata M, Okumura K, Yagita H;
DR WPI; 96-443140/44.
DR N-PSDB; T39550.
PT Monoclonal antibody specifically recognising the Fas ligand - useful
PT for the detection of Fas ligands either on cell surface or in
PT solution
PS Claim 20; Pages 80-81; 133pp; Japanese.
CC The present sequence is a variant light chain variable region
CC of the anti-human Fas ligand monoclonal antibody (MAb) NOK-1. NOK-1
CC is produced by the hybridoma NOK-1 (FERM BP-5044), which was
CC prepared by immunising mice with transformed human Fas ligand
CC expressing COS cells, and fusing spleen cells isolated from the
CC mice with myeloma P3x63Ag8.653 (ATCC CRL-1580) cells. The MAb
CC recognises the human Fas ligand on the cell surface or in solution,
CC and can be used to inhibit the apoptosis inducing cell surface Fas
CC ligand/Fas reaction. The MAb can also be used for a Fas ligand
CC assay in biological samples (e.g. human blood), especially for
CC disease diagnosis, e.g. hepatitis, infectious mononucleosis and
CC systemic lupus erythematosus.
SQ Sequence 108 AA;

Query Match   100.0%;   Score 51;   DB 20;   Length 108;
Best Local Similarity 100.0%;   Pred. No. 5.83e+00;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   50 ytsrlhs 56
     ||||||
Qy   1 YTSRLHS 7

RESULT 5
ID R52039 standard; Protein; 109 AA.
AC R52039;
DT 27-SEP-1996 (first entry)
DE Light chain variable region of murine antibody 1f19.
KW antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify.
OS Mus sp.
FH Key   Location/Qualifiers
FT Region   1..23
FT /label- framework_region_1
FT /note- "FR 1"
FT Region   24..34
FT /label- complementarity_determining_region_1
FT /note- "CDR 1"
FT Region   35..49
FT /label- FR_2
FT Region   50..56

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FT   /label= CDR_2
FT   Region         57..88
FT   /label= FR_3
FT   Region         89..97
FT   /label= CDR_3
FT   Region         98..109
FT   /label= FR_4
PN   EP-592106-A1.
PD   13-APR-1994.
PF   07-SEP-1993; 307051.
PR   09-SEP-1992; US-942245.
PA   (PEDE/) PEDERSEN J T.
PA   (IMMU-) IMMUNOGEN INC.
PI   Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
DR   WPI; 94-120230/15.
PT   Method of resurfacing of rodent antibodies to produce humanised
PT   antibody forms - for producing non-human antibodies with improved
PT   therapeutic efficiency by presenting human surface on V-region
PS   Example 1; Fig 3A; 230pp; English.
CC   The present sequence is that of the light chain variable (LC VR) region
CC   of murine antibody 1f19. This sequence was aligned with 11 other known
CC   antibody LC VRs and a set of framework positions of surface exposed amino
CC   acid residues was determined. This information can be used in a method to
CC   determine how to modify a rodent antibody or fragment by resurfacing in
CC   order to produce a humanised rodent antibody. Residues (determined from
CC   alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
CC   87, 111, 115, 116 and 117 are accessible residues. None of the entire
CC   combinations of surface residues in the murine sequences were found in
CC   the human sequences and vice versa. However the residues in individual
CC   positions appear to be conserved.
SQ   Sequence   109 AA;

Query Match            100.0%;    Score 51;    DB 17;   Length 109;
Best Local Similarity  100.0%;    Pred. No. 5.83e+00;
Matches      7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   50 ytsrlhs 56
        |||||||
Qy    1 YTSRLHS  7

RESULT   6
ID   R47206 standard; Protein; 124 AA.
AC   R47206;
DT   09-AUG-1994 (first entry)
DE   Human/murine IL-1 chimeric antibody CH.
KW   Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;
KW   light; L; chain; constant; region; variable; mouse; anti-human;
KW   graft; CDR; complementarity determining region; heavy; H;
KW   inflammatory disease; arteriosclerosis; leukemia.
OS   Synthetic.
FH   Key          Location/Qualifiers
FT   Peptide        1..17
FT   /note= "Signal peptide"
FT   Protein       18..124
FT   /note= "Mature protein"
PN   WO9402627-A.
PD   03-FEB-1994.
PF   08-JUL-1993; J00941.
PR   16-JUL-1992; JP-189248.
PA   (SAKA ) OTSUKA PHARM CO LTD.
PI   Hirai Y, Nishida T, Omoto Y, Owens RJ;
DR   WPI; 94-048885/06.
DR   N-PSDB; Q56067.
PT   Mouse/human chimeric antibody against human interleukin-1 - for
PT   treatment of diseases in which production of interleukin-1 is
PT   abnormal, and for diagnostic imaging of interleukin-1 production
PT   sites in vivo
PS   Claim 1; Page 31-32; 58pp; Japanese.
CC   The sequences given in R47205-08 represent the light and heavy chain,
CC   variable and constant regions of a chimeric recombinant antibody
CC   against human interleukin-1 (IL-1). The antibody has a light (L)
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```
CC   chain in which the constant region is that of a human antibody and
CC   the variable region is from a mouse anti-human IL-1 antibody or is a
CC   mouse-human graft containing the CDR regions of mouse anti-human IL-1
CC   antibody, and a heavy (H) chain in which the constant region is that
CC   of a human antibody and the variable region is from a mouse anti-human
CC   IL-1 antibody or is a mouse-human graft containing the CDR regions of
CC   mouse anti-human IL-1 antibody,. The chimeric antibody is used to
CC   treat diseases in which abnormal amounts of IL-1 are produced, eg.
CC   inflammatory disease, arteriosclerosis, diffused intravascular
CC   coagulation or leukemia. It can also be labelled and used for
CC   diagnostic imaging of IL-1 producing sites in vivo.
SQ   Sequence   124 AA;

Query Match            100.0%;    Score 51;    DB 9;   Length 124;
Best Local Similarity  100.0%;    Pred. No. 5.83e+00;
Matches      7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   67 ytsrlhs 73
        |||||||
Qy    1 YTSRLHS  7

RESULT   7
ID   R29015 standard; Protein; 126 AA.
AC   R29015;
DT   30-MAR-1993 (first entry)
DE   pUC-RV1-PM1a.
KW   Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW   complementarity determining region; mouse; monoclonal; hybridoma;
KW   plasmid; polymerase chain reaction; amplify.
OS   Synthetic.
FH   Key          Location/Qualifiers
FT   Peptide        1..19
FT   /note= "Leader peptide"
FT   Region        20..42
FT   /label= FR1
FT   Region        43..53
FT   /label= CDR1
FT   Region        54..68
FT   /label= FR2
FT   Region        69..75
FT   /label= CDR2
FT   Region        76..107
FT   /label= FR3
FT   Region       108..116
FT   /label= CDR3
FT   Region       117..126
FT   /label= FR4
PN   WO9219759-A.
PD   12-NOV-1992.
PF   24-APR-1992; J00544.
PR   25-APR-1991; JP-095476.
PR   19-FEB-1992; JP-032084.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR   WPI; 92-398882/48.
DR   N-PSDB; Q31366.
PT   Reconstituted human antibody to human interleukin-6 receptor -
PT   has low antigenicity and contains mouse V-region complementarity
PT   determining regions
PS   Disclosure; Page 144-5; 207pp; Japanese.
CC   The sequences given in R29012-15 are portions of monoclonal antibodies
CC   which were encoded by plasmids derived from mouse hybridomas. The DNA
CC   encoding complementarity determining regions (CDR's) was isolated by
CC   polymerase chain reaction. These antibodies recognise human
CC   interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
CC   transformed with the plasmids encoding these genes which caused the
CC   secretion of these antibodies from the hybridoma cells.
SQ   Sequence   126 AA;

Query Match            100.0%;    Score 51;    DB 5;   Length 126;
Best Local Similarity  100.0%;    Pred. No. 5.83e+00;
Matches      7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
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Db        69 ytsrlhs 75
            |||||||
Qy         1 YTSRLHS 7

RESULT     8
ID    R29013 standard; Protein; 126 AA.
AC    R29013;
DT    30-MAR-1993 (first entry)
DE    pUC-RVh-PM1a.
KW    Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW    complementarity determining region; mouse; monoclonal; hybridoma;
KW    plasmid; polymerase chain reaction; amplify.
OS    Synthetic.
FH    Key            Location/Qualifiers
FT    Peptide        1..19
FT    /note="Leader peptide"
FT    Region         20..42
FT    /label- FR1
FT    Region         43..53
FT    /label- CDR1
FT    Region         54..68
FT    /label- FR2
FT    Region         69..75
FT    /label- CDR2
FT    Region         76..107
FT    /label- FR3
FT    Region         108..116
FT    /label- CDR3
FT    Region         117..126
FT    /label- FR4
PN    WO9219759-A.
PD    12-NOV-1992.
PF    24-APR-1992; J00544.
PR    25-APR-1991; JP-095476.
PR    19-FEB-1992; JP-032084.
PA    (CHUS ) CHUGAI SEIYAKU KK.
PI    Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR    WPI; 92-398882/48.
DR    N-PSDB; Q31361.
PT    Reconstituted human antibody to human interleukin-6 receptor -
PT    has low antigenicity and contains mouse V-region complementarity
PT    determining regions
CC    Disclosure: Page 140-1; 207pp; Japanese.
CC    The sequences given in R29012-15 are portions of monoclonal antibodies
CC    which were encoded by plasmids derived from mouse hybridomas. The DNA
CC    encoding complementarity determining regions (CDR's) was isolated by
CC    polymerase chain reaction. These antibodies recognise human
CC    interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
CC    transformed with the plasmids encoding these genes which caused the
CC    secretion of these antibodies from the hybridoma cells.
SQ    Sequence  126 AA;

Query Match             100.0%;         Score 51;  DB 5;  Length 126;
Best Local Similarity   100.0%;         Pred. No. 5.83e+00;
Matches     7;    Conservative     0;    Mismatches    0;   Indels    0;   Gaps   0;

Db        69 ytsrlhs 75
            |||||||
Qy         1 YTSRLHS 7

RESULT     9
ID    W11815 standard; Protein; 127 AA.
AC    W11815;
DT    20-OCT-1997 (first entry)
DE    Mouse anti-human Fas ligand antibody F919 light chain.
KW    Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
KW    induction; assay; enzyme linked immunosorbant assay; diagnosis;
KW    disease; hepatitis B; hepatitis C; human immunodeficiency virus;
KW    graft versus host disease; ulcerative colitis; sequelae;
KW    myocardial infarction; mouse; murine; monoclonal; treatment;
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KW    complementarity determining region; CDR.
OS    Mus spp.
FH    Key            Location/Qualifiers
FT    Region         44..54
FT    /label- CDR_1
FT    Region         70..76
FT    /label- CDR_2
FT    Region         109..117
FT    /label- CDR_3
PN    WO9702290-A1.
PD    23-JAN-1997.
PF    01-JUL-1996; J01820.
PR    17-MAY-1996; US-649100.
PR    30-JUN-1995; JP-188480.
PA    (MOCH ) MOCHIDA PHARM CO LTD.
PA    (OSAB-) OSAKA BIOSCIENCE INST.
PI    Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
DR    WPI; 97-108917/10.
DR    N-PSDB; T59500.
PT    Antibody reactive with Fas ligand capable of inducing apoptosis -
PT    used for diagnostic assay of Fas ligand in body fluids and for
PT    treatment of diseases in which Fas ligand/Fas antigen is involved
PS    Claim 5; Fig 10; 164pp; Japanese.
CC    The present sequence is the light chain of the mouse
CC    anti-apoptosis inducing human Fas ligand, monoclonal antibody,
CC    F919. The antibody can be used in a Fas ligand assay, e.g. an
CC    enzyme linked immunosorbant assay, to diagnose diseases in which
CC    the Fas ligand/Fas antigen system is implicated, e.g. hepatitis
CC    B/C, human immunodeficiency virus, graft/host disorders,
CC    ulcerative colitis or sequelae of myocardial infarction. The
CC    antibody may also be used to treat such diseases.
SQ    Sequence  127 AA;

Query Match             100.0%;         Score 51;  DB 22;  Length 127;
Best Local Similarity   100.0%;         Pred. No. 5.83e+00;
Matches     7;    Conservative     0;    Mismatches    0;   Indels    0;   Gaps   0;

Db        70 ytsrlhs 76
            |||||||
Qy         1 YTSRLHS 7

RESULT     10
ID    W11817 standard; Protein; 127 AA.
AC    W11817;
DT    20-OCT-1997 (first entry)
DE    Humanised mouse anti-human Fas ligand antibody F919 light chain.
KW    Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
KW    induction; assay; enzyme linked immunosorbant assay; diagnosis;
KW    disease; hepatitis B; hepatitis C; human immunodeficiency virus;
KW    graft versus host disease; ulcerative colitis; sequelae; chimeric;
KW    myocardial infarction; mouse; murine; monoclonal; treatment.
OS    Chimeric - Mus spp.
OS    Chimeric - Homo sapiens.
OS    Synthetic.
FH    Key            Location/Qualifiers
FT    Region         44..54
FT    /label- CDR_1
FT    Region         70..76
FT    /label- CDR_2
FT    Region         109..117
FT    /label- CDR_3
PN    WO9702290-A1.
PD    23-JAN-1997.
PF    01-JUL-1996; J01820.
PR    17-MAY-1996; US-649100.
PR    30-JUN-1995; JP-188480.
PA    (MOCH ) MOCHIDA PHARM CO LTD.
PA    (OSAB-) OSAKA BIOSCIENCE INST.
PI    Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
DR    WPI; 97-108917/10.
DR    N-PSDB; T59502.
PT    Antibody reactive with Fas ligand capable of inducing apoptosis -
```

PT used for diagnostic assay of Fas ligand in body fluids and for
PT treatment of diseases in which Fas ligand/Fas antigen is involved
PS Claim 5; Fig 12; 164pp; Japanese.
CC The present sequence is the light chain of the humansied
CC mouse anti-apoptosis inducing human Fas ligand, monoclonal
CC antibody, F919. The antibody can be used in a Fas ligand assay,
CC e.g. an enzyme linked immunosorbant assay, to diagnose diseases
CC in which the Fas ligand/Fas antigen system is implicated, e.g.
CC hepatitis B/C, human immunodeficiency virus; graft/host disorders,
CC ulcerative colitis or sequelae of myocardial infarction. The
CC antibody may also be used to treat such diseases.
SQ Sequence 127 AA;

Query Match   100.0%; Score 51; DB 22; Length 127;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   70 ytsrlhs 76
           |||||||
Qy   1 YTSRLHS 7

RESULT 11
ID   R28670 standard; Protein; 127 AA.
AC   R28670;
DT   30-MAR-1993 (first entry)
DE   pPM-k3 protein product.
KW   Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW   heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
KW   plasmid; pPM-k3; pPM-hl.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   Peptide   1..20
FT   /note= "Signal peptide"
FT   Protein   21..127
FT   /note= "Mature peptide"
PN   WO9219759-A.
PD   12-NOV-1992.
PF   24-APR-1992; J00544.
PR   25-APR-1991; JP-095476.
PR   19-FEB-1992; JP-032084.
PA   (CHUS) CHUGAI SEIYAKU KK.
PI   Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR   WPI; 92-398882/48.
DR   N-PSDB: Q30755.
PT   Reconstituted human antibody to human interleukin-6 receptor -
PT   has low antigenicity and contains mouse V-region complementarity
PT   determining regions
PS   Disclosure; Page 121-122; 207pp; Japanese.
CC   The sequences given in R28670-71 were encoded by plasmids which were
CC   used in example to illustrate the production of a human antibody which
CC   recognises human interleukin-6 receptor (IL-6R). The antibody
CC   comprises light (L) chain and heavy (H) chain variable regions which
CC   were derived from a mouse monoclonal antibody produced from the
CC   hybridoma PM1 which contained the plasmids pPM-k3 and pPM-hl.
SQ   Sequence 127 AA;

Query Match   100.0%; Score 51; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   70 ytsrlhs 76
           |||||||
Qy   1 YTSRLHS 7

RESULT 12
ID   R32121 standard; Protein; 127 AA.
AC   R32121;
DT   02-JUN-1993 (first entry)
DE   Anti-CD4 antibody MT 15.1 light chain variable region.
KW   immunosuppression; tissue transplantation; graft; L chain; V region;
KW   T-helper cell inhibition; transplant rejection; MAb;

KW   interleukin-2 receptor.
FH   Key   Location/Qualifiers
FT   Peptide   1..20
FT   /label- signal
FT   Region   21..115
FT   /label- Variable
FT   Region   116..127
FT   /label= J2
PN   DE4143214-A.
PD   28-JAN-1993.
PF   30-DEC-1991; 143214.
PR   25-JUL-1991; DE-124759.
PR   30-DEC-1991; DE-143214.
PA   (BOEF) BOEHRINGER MANNHEIM GMBH.
PI   Kaluza B, Riethmueller G, Scheuer W, Weidle U;
DR   WPI; 93-037582/05.
DR   N-PSDB: Q36607.
PT   Synergistic antibody compsn. for use as immunosuppressant -
PT   comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT   alpha- or anti-IL2R beta antibodies
PS   Claim 5; Page 9; 18pp; German.
CC   This sequence is the light chain variable region of a preferred
CC   anti-CD4 monoclonal antibody for use in the claimed synergistic
CC   composition. MAb MT 15.1 is deposited as clone 15-1/P3/14 (ECACC
CC   90090705). The anti-CD4 antibody is used with at least one anti-IL2R
CC   alpha or beta antibody. Individually the antibodies are strongly
CC   inhibiting and when used together their immunosuppresive properties
CC   are improved; they synergistically inhibit T-helper cell
CC   proliferation to effectively inhibit transplant rejection at low
CC   doses without significantly reducing the general immune response.
CC   See also Q36608-Q36616.
SQ   Sequence 127 AA;

Query Match   100.0%; Score 51; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   70 ytsrlhs 76
           |||||||
Qy   1 YTSRLHS 7

RESULT 13
ID   W06215 standard; Protein; 128 AA.
AC   W06215;
DT   13-FEB-1997 (first entry)
DE   MAb ME4 light chain variable region.
KW   Chimeric antibody; monoclonal antibody; ME4; antibody engineering;
KW   tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
KW   ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.
OS   Mus sp.
PN   US5576184-A.
PD   19-NOV-1996.
PF   06-SEP-1988; 240624.
PR   06-SEP-1988; US-240624.
PR   06-SEP-1988; US-240744.
PR   08-SEP-1988; US-241744.
PR   13-SEP-1988; US-243739.
PR   04-OCT-1988; US-253002.
PR   19-JUN-1989; US-367641.
PR   21-JUL-1989; US-382768.
PR   06-MAY-1991; US-659401.
PR   27-DEC-1994; US-364001.
PA   (XOMA) XOMA CORP.
PI   Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
DR   WPI; 97-01249/01.
DR   N-PSDB: T43440.
PT   Chimeric mouse-human antibodies - recognise a human tumour antigen,
PT   used for the treatment and diagnosis of human cancers
PS   Example 3; Fig 29; 102pp; English.
CC   The light chain variable region (W06215) of mouse monoclonal
CC   antibody ME4 is the product of a cDNA clone (T43340) isolated
CC   from a ME4 hybridoma cDNA library. MAb ME4 (IgG1) binds to an
CC   antigen that is expressed on the surface of human lung, breast,

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CC  colon and ovary carcinomas and melanomas, but not on most normal
CC  adult tissues.  The light chain and heavy chain variable regions
CC  (see also W06216) of ME4 can be linked to human constant regions
CC  and expressed in transformed host cells.  Novel mouse-human
CC  chimeric antibodies (see also W06209-14 and W06217-18) can be
CC  produced that have specificity to human tumour antigens for use in
CC  the treatment and diagnosis of human cancer.
SQ  Sequence  128 AA;

Query Match       100.0%;   Score 51;  DB 19;  Length 128;
Best Local Similarity 100.0%;    Pred. No. 5.83e+00;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db    70 ytsrlhs 76
         |||||||
Qy     1 YTSRLHS 7

RESULT   14
ID  R09426 standard; Protein; 128 AA.
AC  R09426;
DT  04-MAR-1993  (first entry)
DE  ME4 Light Chain V Region (mouse).
KW  Monoclonal antibody; chimera; light; heavy; chain; constant;
KW  variable; antigen; diagnosis; cancer; tumour.
OS  Mus musculus.
PN  WO9002569-A.
PD  22-MAR-1990.
PF  06-SEP-1989;  U03852.
PR  06-SEP-1988; US-240624.
PR  08-SEP-1988; US-241744.
PR  13-SEP-1988; US-243739.
PR  04-OCT-1988; US-253002.
PR  19-JUN-1989; US-367641.
PR  21-JUL-1989; US-382768.
PA  (ITGE-) INT GENETIC ENG INC.
PI  Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
DR  WPI: 90-115825/15.
DR  N-PSDB; Q08608.
PT  Chimeric mouse-human antibodies - prepd. using genes coding for
PT  constant human region murine variable region, esp. to 3 tumour
PT  antigen
PS  Claim 13; Page 123 + Fig 29; 173pp; English.
CC  The sequence is used in the prodn. of a chimeric antibody mol.
CC  comprising two light chains and two heavy chains, each having a
CC  constant region (human) and a variable region (murine) having
CC  specificity to an antigen bound by murine monoclonal antibody
CC  (MAb) ME4.  The chimeric antibodies can be used for any purpose for
CC  which the original murine MAbs can be used, with the advantage that
CC  they are more compatible with the human body.  They are esp. used for
CC  the diagnosis and treatment of cancer.
SQ  Sequence  128 AA;

Query Match       100.0%;   Score 51;  DB 5;  Length 128;
Best Local Similarity 100.0%;    Pred. No. 5.83e+00;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db    70 ytsrlhs 76
         |||||||
Qy     1 YTSRLHS 7

RESULT   15
ID  R47207 standard; Protein; 129 AA.
AC  R47207;
DT  09-AUG-1994  (first entry)
DE  Human/murine IL-1 chimeric antibody VL.
KW  Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;
KW  light; L; chain; constant; region; variable; mouse; anti-human;
KW  graft; CDR; complementarity determining region; heavy; H;
KW  inflammatory disease; arteriosclerosis; detection;
KW  diffused intravascular coagulation; leukemia.
OS  Synthetic.
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FH  Key             Location/Qualifiers
FT  Peptide         1..20
FT  /note= "signal peptide"
FT  Protein         21..129
FT  /note= "mature protein"
PN  WO9402627-A.
PD  03-FEB-1994.
PF  08-JUL-1993; J00941.
    16-JUL-1992; JP-189248.
PA  (SAKA ) OTSUKA PHARM CO LTD.
PI  Hirai Y, Nishida T, Omoto Y,  Owens RJ;
DR  WPI; 94-048885/06.
DR  N-PSDB; Q56068.
PT  Mouse/human chimeric antibody against human interleukin-1 - for
PT  treatment of diseases in which production of interleukin-1 is
PT  abnormal, and for diagnostic imaging of interleukin-1 production
PT  sites in vivo
PS  Claim 2; Fig 10; 58pp; Japanese.
CC  The sequences given in R47205-08 represent the light and heavy chain,
CC  variable and constant regions of a chimeric recombinant antibody
CC  against human interleukin-1 (IL-1).  The antibody has a light (L)
CC  chain in which the constant region is that of a human antibody and
CC  the variable region is from a mouse anti-human IL-1 antibody or is a
CC  mouse-human graft containing the CDR regions of mouse anti-human IL-1
CC  antibody, and a heavy (H) chain in which the constant region is that
CC  of a human antibody and the variable region is from a mouse anti-human
CC  IL-1 antibody or is a mouse-human graft containing the CDR regions of
CC  mouse anti-human IL-1 antibody,.  The chimeric antibody is used to
CC  treat diseases in which abnormal amounts of IL-1 are produced, eg.
CC  inflammatory disease, arteriosclerosis, diffused intravascular
CC  coagulation or leukemia.  It can also be labelled and used for
CC  diagnostic imaging of IL-1 producing sites in vivo.
SQ  Sequence  129 AA;

Query Match       100.0%;   Score 51;  DB 9;  Length 129;
Best Local Similarity 100.0%;    Pred. No. 5.83e+00;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db    70 ytsrlhs 76
         |||||||
Qy     1 YTSRLHS 7

RESULT   16
ID  R84553 standard; Protein; 131 AA.
AC  R84553;
DT  02-FEB-1996  (first entry)
DE  MAb SCH94.03 light chain.
KW  Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system;
KW  CNS; demyelination; multiple sclerosis; neural disease; therapeutic.
OS  Mus sp.
FH  Key             Location/Qualifiers
FT  Peptide         1..20
FT  /label= Leader_peptide
FT  Region          44..54
FT  /label- CDR1
FT  Region          70..76
FT  /label- CDR2
FT  Region          109..117
FT  /label- CDR3
FT  Region          116..128
FT  /label- Joining_region
FT  Region          129..131
FT  /label- C-kappa_region
PN  WO9530004-A1.
PD  09-NOV-1995.
PF  27-APR-1995; U05262.
PR  29-APR-1994; US-236520.
PA  (MAYO-) MAYO FOUNDATION.
PI  Miller DJ, Rodriguez M;
DR  WPI; 95-393077/50.
DR  N-PSDB; T05311.
PT  Monoclonal antibodies which stimulate central nervous system
```

PT   re-myelination - are produced by hybridoma ATCC CRL 11627, for
PT   treating multiple sclerosis, and viral or post-neural diseases of
PT   the CNS.
PS   Disclosure; Page 36-37; 63pp; English.
CC   Hybridoma ATCC CRL 11627 was obtd. from a SJL/J mouse injected with
CC   spinal cord homogenate from a mammal uninfected with any
CC   demyelinating disease. The hybridoma produced a monoclonal antibody
CC   (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
CC   light chain amino acid sequence is given in R84553.
SQ   Sequence 131 AA;

Query Match   100.0%; Score 51; DB 14; Length 131;
Best Local Similarity   100.0%; Pred. No. 5.83e+00;
  Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   70 ytsrlhs 76
              |||||||
Qy   1 YTSRLHS 7

RESULT 17
ID   R44226 standard; protein; 268 AA.
AC   R44226;
DT   10-JUN-1994 (first entry)
DE   Chimeric Ig superfamily protein analogue R19(D1.3).
KW   CHI-protein; Immunoglobulin superfamily; multivalent antigen binding;
KW   engineered fusion protein; beta-barrel domain; chimaeric;
KW   complementarity determining region; cell imaging; targetting.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   Region   1..30
FT   /label= H_FR1
FT   /note= "Heavy chain framework region from R19.9"
FT   Region   31..35
FT   /label= H1
FT   /note= "primary CDR loop from R19.9"
FT   Region   36..39
FT   /label= FR2A
FT   /note= "Heavy chain framework region from R19.9"
FT   Region   40..45
FT   /label= H3'
FT   /note= "CDR loop spliced into chi-site from D1.3"
FT   Region   46..48
FT   /label= FR2B
FT   /note= "Heavy chain framework region from R19.9"
FT   Region   49..65
FT   /label= H2
FT   /note= "primary CDR loop from R19.9"
FT   Region   66..89
FT   /label= H_FR3A
FT   /note= "Heavy chain framework region from R19.9"
FT   Region   90..92
FT   /label= H1'
FT   /note= "CDR loop spliced into chi-site from D1.3"
FT   Region   93..97
FT   /label= H_FR3B
FT   /note= "Heavy chain framework region from R19.9"
FT   Region   98..112
FT   /label= H3
FT   /note= "primary CDR loop from R19.9"
FT   Region   113..116
FT   /label= H_FR4
FT   /note= "Heavy chain framework region from R19.9"
FT   Region   117..135
FT   /label= H2'
FT   /note= "CDR loop spliced into chi-site from D1.3"
FT   Region   136..155
FT   /label= "bridge/linker"
FT   Region   156..178
FT   /label= L_FR1
FT   /note= "Light chain framework region from R19.9"
FT   Region   179..189
FT   /label= L1

FT   /note= "primary CDR loop from R19.9"
FT   Region   190..193
FT   /label= FR2A
FT   /note= "Light chain framework region from R19.9"
FT   Region   194..199
FT   /label= L3'
FT   /note= "CDR loop spliced into chi-site from D1.3"
FT   Region   200..203
FT   /label= FR2B
FT   /note= "Light chain framework region from R19.9"
FT   Region   204..210
FT   /label= L2
FT   /note= "primary CDR loop from R19.9"
FT   Region   211..237
FT   /label= L_FR3A
FT   /note= "Light chain framework region from R19.9"
FT   Region   238..241
FT   /label= L1'
FT   /note= "CDR loop spliced into chi-site from D1.3"
FT   Region   242..244
FT   /label= FR3B
FT   /note= "Light chain framework region from R19.9"
FT   Region   245..253
FT   /label= L3
FT   /note= "primary CDR loop from R19.9"
FT   Region   254..255
FT   /label= FR4
FT   /note= "Light chain framework region from R19.9"
FT   Region   256..268
FT   /label= L2'
FT   /note= "CDR loop spliced into chi-site from D1.3"
PN   WO9323537-A.
PD   25-NOV-1993.
PF   07-MAY-1993; U04338.
PR   08-MAY-1992; US-881109.
PA   (CREA-) CREATIVE BIOMOLECULES.
PI   Huston JS, Keck PC;
DR   WPI; 93-386569/48.
PT   Chimeric multivalent protein analogues - useful for diagnostic
PT   imaging and cytotoxic therapy.
PS   Example 1; Fig 14; 106pp; English.
CC   This sequence is an example of a CHI-protein constructed according
CC   to the invention. The novel CHI (Chimeric immunoglobulin)-proteins
CC   are comprised of at least 1 beta-barrel forming domain. The antigen
CC   binding sites of the molecule are located in the beta-barrel
CC   domain(s). Splice sites for insertion of specific binding sites are
CC   located by computer comparisons of homology and structure. Depending
CC   on the ligand binding specificity of the chimeric molecules, they
CC   can be targetted for imaging, irradiating or delivering cytotoxic
CC   substances to specific tissues.
SQ   Sequence 268 AA;

Query Match   100.0%; Score 51; DB 8; Length 268;
Best Local Similarity   100.0%; Pred. No. 5.83e+00;
  Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   204 ytsrlhs 210
              |||||||
Qy   1 YTSRLHS 7

RESULT 18
ID   R60206 standard; protein; 302 AA.
AC   R60206;
DT   14-MAR-1995 (first entry)
DE   Bispecific CD3-L6FvIg antibody derivative.
KW   fusion protein; recombinant bispecific single chain antibody;
KW   helical peptide linker; anti-L6 antibody; tumour cell antigen;
KW   anti-CD3 antibody; variable region.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   Peptide   1..23
FT   /label= L6_VL_leader

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FT   Region          24..271
FT   /label- CD3_VL-VH_fusion
FT   Region          134..148
FT   /label- (Gly4Ser)3_linker
FT   Region          272..274
FT   /label- hinge
FT   Region          275..302
FT   /label- Fv_helical_linker
PN   EP-610046-A.
PD   10-AUG-1994.
PF   31-JAN-1994; 300692.
PR   01-FEB-1993; US-013420.
PR   13-SEP-1993; US-121054.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PI   Bajorath J,  Fell PH,  Gilliland LK,  Hayden MS,  Ledbetter JA;
PI   Linsley PS;
DR   WPI; 94-250085/31.
DR   N-PSDB; Q81076.
PT   Expression vector encoding bispecific fusion protein - having
PT   binding domains for separate targets joined by helical peptide,
PT   useful e.g. for diagnosis and treatment
PS   Example 1; Fig 11 and Page 29-31; 50pp; English.
CC   The VL and VH sequences of the anti-CD3 hybridoma G19-4 were
CC   amplified by PCR methods. A gene fusion was constructed from the
CC   two amplified domains and a (Gly4Ser)3 linker. The amino
CC   terminus of the VL-VH fusion cassette was fused at the SalI site to
CC   the L6 light chain variable region leader peptide and the
CC   carboxy-terminus was fused directly to the hinge region of the Fc
CC   domain at the BclI site and/or to a short "helical" peptide linker
CC   to construct the bispecific CD3-L6FvIg antibody derivative. The
CC   variable regions for L6 were fused in frame to the opposite end of
CC   the helical linker (not included in R60206).
SQ   Sequence   302 AA;

Query Match           100.0%;  Score 51;  DB 10;  Length 302;
Best Local Similarity 100.0%;  Pred. No. 5.83e+00;
Matches       7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db   73 ytsrlhs 79
        |||||||
Qy    1 YTSRLHS 7


RESULT   19
ID   R99003 standard; Protein; 127 AA.
AC   R99003;
DT   10-JAN-1997  (first entry)
DE   MAb VL17E6 light chain (specific for human alphaV integrins).
KW   Monoclonal antibody; MAb; integrin; cell-matrix interaction;
KW   tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
KW   imaging; detection; radiolabel.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Region          21..43
FT   /label- Framework region 1
FT   Binding_site    44..54
FT   /label- CDR1
FT   Region          55..69
FT   /label- Framework region 2
FT   Binding_site    70..76  .
FT   /label- CDR2
FT   Region          77..108
FT   /label- Framwork region 3
FT   Binding_site    109..117
FT   /label- CDR3
FT   Region          118..127
FT   /label- Framework region 4
PN   EP-719859-A1.
PD   03-JUL-1996.
PF   06-DEC-1995; 119233.
PR   20-DEC-1994; EP-120165.
PA   (MERE ) MERCK PATENT GMBH.
PI   Adan J, Goodman S,  Hahn D,  Mitjans F,  Piulats J;
PI   Rosell E;
DR   WPI; 96-302345/31.
DR   N-PSDB; T35050.
PT   New human integrin V chain-specific monoclonal antibody - and
PT   related DNA and hybridomas, for treatment and diagnostic imaging of
PT   tumours, esp melanoma.
PS   Claim 8; Figure 17a; 54pp; English.
CC   A monoclonal antibody which reacts only with the alphaV chain of
CC   human alphaV integrins; which blocks attachment of alphaV integrin
CC   bearing cells to integrin substrate; which reverses established cell
CC   matrix interactions caused by alphaV integrin; which blocks tumour
CC   development and which has no cytotoxic activity, may be used to
CC   treat tumours, especially melanoma (but also glioma, carcinoma)
CC   optionally coupled to a cytokine such as interleukin-2. The
CC   monoclonal antibody may also be used for diagnostic imaging of
CC   tumours and assesment of tumour growth when conjugated to a
CC   radiolabel or a radio opaque-agent.
SQ   Sequence   127 AA;

Query Match           90.2%;   Score 46;  DB 19;  Length 127;
Best Local Similarity 85.7%;   Pred. No. 2.76e+01;
Matches       6;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db   70 ytsklhs 76
        ||| ||||
Qy    1 YTSRLHS 7

Search completed: Tue Mar  3 14:28:25 1998
Job time : 17 secs.
```

```
 _ _ _ _ _ _ _ _ _ _ _ _ _
|\ /||_) (_  |_) /  |_|
| V || \ _)  | \ \_ | |  (TM)
```

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 3 14:32:15 1998; MasPar time 2.93 Seconds
                                         72.785 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117D-118
Description: (1-7) from US08137117D.pep
Perfect Score: 51
Sequence: 1 YTSRLHS 7

Scoring table: PAM 150
               Gap 15

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: pir53
               1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
               8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
               13:unann9 14:unann10 15:unann10 16:unann11 17:unenc
               18:unrev

Statistics: Mean 20.894; Variance 23.719; scale 0.881

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES

                         %
Result   Query
No.   Score   Match Length DB ID   Description   Pred. No.
---- ----- ------ ------ -- ------   -----------   ---------
  1   51   100.0   93   7   S38564   Ig light chain V reg   2.38e-01
  2   51   100.0   107   7   B48677   Ig light chain V-J r   2.38e-01
  3   51   100.0   107   7   S69901   Ig kappa light chain   2.38e-01
  4   51   100.0   107   7   S69906   Ig kappa light chain   2.38e-01
  5   51   100.0   107   7   B28044   Ig kappa chain V reg   2.38e-01
  6   51   100.0   107   7   B49026   Ig kappa chain V reg   2.38e-01
  7   51   100.0   107   7   A28044   Ig kappa chain V reg   2.38e-01
  8   51   100.0   107   7   C48677   Ig light chain V-J r   2.38e-01
  9   51   100.0   107   7   D48677   Ig light chain V-J r   2.38e-01
 10   51   100.0   108   7   S69902   Ig kappa light chain   2.38e-01
 11   51   100.0   108   7   S69903   Ig kappa light chain   2.38e-01
 12   51   100.0   108   2   KVMSAR   Ig kappa chain V reg   2.38e-01
 13   51   100.0   108   7   S38862   Ig kappa light chain   2.38e-01
 14   51   100.0   108   7   S69900   Ig kappa chain V reg   2.38e-01
 15   51   100.0   108   7   S19970   Ig kappa chain V reg   2.38e-01
 16   51   100.0   109   7   PH0888   Ig light chain V-J r   2.38e-01
 17   51   100.0   115   7   A53276   Ig kappa chain V reg   2.38e-01
 18   51   100.0   115   7   JL0080   Ig light chain precu   2.38e-01
 19   51   100.0   122   7   A29380   Ig kappa chain precu   2.38e-01
 20   51   100.0   127   7   PH1224   Ig kappa chain precu   2.38e-01
 21   51   100.0   128   7   A26406   Ig kappa chain V reg   2.38e-01
 22   48   94.1   107   7   A48677   Ig light chain V-J r   1.21e+00
 23   48   94.1   470   9   S02068   RNA-directed RNA pol   1.21e+00
 24   48   94.1   529   9   A24031   genome polyprotein -   1.21e+00
 25   48   94.1   2332   4   GNNY4F   genome polyprotein -   1.21e+00
 26   48   94.1   2332   4   GNNYF   genome polyprotein -   1.21e+00
 27   48   94.1   2333   4   GNNY2F   genome polyprotein -   1.21e+00
 28   46   90.2   126   7   A34904   Ig kappa chain precu   3.44e+00
 29   45   88.2   470   9   JN0431   RNA-directed RNA pol   5.75e+00
 30   45   88.2   473   18   S53119   RNA-dependent RNA po   5.75e+00
 31   45   88.2   2336   9   S37077   genome polyprotein -   5.75e+00
 32   44   86.3   105   7   PH0087   Ig kappa chain V reg   9.53e+00
 33   44   86.3   178   2   TVRTBM   transforming protein   9.53e+00
 34   44   86.3   230   16   S33161   Ig kappa chain - she   9.53e+00
 35   44   86.3   502   8   A23547   keratin, type II cyt   9.53e+00
 36   43   84.3   847   14   JC4836   alpha-glucuronidase   1.57e+01
 37   43   84.3   975   14   B34751   hypothetical protein   1.57e+01
 38   42   82.4   107   7   S32188   Ig kappa chain V reg   2.55e+01
 39   42   82.4   274   13   S17923   rbcL intron protein   2.55e+01
 40   42   82.4   334   12   I39843   iron-uptake system c   2.55e+01
 41   42   82.4   721   13   S49789   hypothetical protein   2.55e+01
 42   42   82.4   747   13   S69557   hypothetical protein   2.55e+01
 43   42   82.4   787   13   S56268   hypothetical protein   2.55e+01
 44   42   82.4   961   15   A55380   faciogenital dysplas   2.55e+01
 45   41   80.4   111   7   E38740   Ig kappa chain V reg   4.13e+01

                                    ALIGNMENTS

RESULT   1
ENTRY   S38564   #type fragment
TITLE   Ig light chain v region (ASWU1) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
              09-May-1997
ACCESSIONS   S38564
REFERENCE   S38559
  #authors   Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
  #submission submitted to the EMBL Data Library, September 1993
  #description Molecular analysis of mercury-induced anti-nucleolar
              antibodies in H-2s Mice.
  #accession S38564
    ##status preliminary
    ##molecule_type mRNA
    ##residues 1-93 ##label MON
    ##cross-references EMBL:X75105
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS   immunoglobulin
SUMMARY   #length 93 #checksum 1511

Query Match   100.0%;   Score 51; DB 7; Length 93;
Best Local Similarity 100.0%; Pred.No. 2.38e-01;
Matches   7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   50 ytsrlhs 56
          |||||||
Qy   1 YTSRLHS 7

RESULT   2
ENTRY   B48677   #type fragment
TITLE   Ig light chain V-J region (44.1) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   19-May-1994 #sequence_revision 19-May-1994 #text_change
              16-Aug-1996
ACCESSIONS   B48677
REFERENCE   A48677
  #authors   Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
              P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
  #journal   Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
  #title   Molecular characterization of monoclonal CRI-A-positive
              anti-arsonate antibodies derived from idiotype-negative
              mice bearing a light chain polymorphism.
```

```
#accession    B48677
  ##status      preliminary; not compared with conceptual translation
  ##molecule_type mRNA
  ##residues    1-107 ##label TAS
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS      immunoglobulin
SUMMARY       #length 107 #checksum 9096

Query Match     100.0%;    Score 51;  DB 7; Length 107;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db        50 ytsrlhs 56
             |||||||
Qy         1 YTSRLHS 7

RESULT     3
ENTRY      S69901        #type complete
TITLE      Ig kappa light chain (clone KL2.21) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
           09-May-1997
ACCESSIONS S69901
REFERENCE  S69900
  #authors   Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
  #journal   Immunology (1992) 75:116-121
  #title     B-cell proliferation initiated by Ia cross-linking and
             sustained by interleukins leads to class switching but not
             somatic mutation in vitro.
  #accession S69901
  ##status      preliminary; translation not shown
  ##molecule_type DNA
  ##residues    1-107 ##label WYS
  ##cross-references EMBL:X55042
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
SUMMARY       #length 107 #molecular-weight 11857 #checksum 7740

Query Match     100.0%;    Score 51;  DB 7; Length 107;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db        50 ytsrlhs 56
             |||||||
Qy         1 YTSRLHS 7

RESULT     4
ENTRY      S69906        #type complete
TITLE      Ig kappa light chain (clone KL4A1) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
           09-May-1997
ACCESSIONS S69906
REFERENCE  S69900
  #authors   Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
  #journal   Immunology (1992) 75:116-121
  #title     B-cell proliferation initiated by Ia cross-linking and
             sustained by interleukins leads to class switching but not
             somatic mutation in vitro.
  #accession S69906
  ##status      preliminary; translation not shown
  ##molecule_type DNA
  ##residues    1-107 ##label WYS
  ##cross-references EMBL:X55047
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
SUMMARY       #length 107 #molecular-weight 11827 #checksum 7550

Query Match     100.0%;    Score 51;  DB 7; Length 107;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db        50 ytsrlhs 56
```

```
Qy         1 YTSRLHS 7
             |||||||

RESULT     5
ENTRY      B28044        #type complete
TITLE      Ig kappa chain v region (GP1) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       19-May-1989 #sequence_revision 19-May-1989 #text_change
           16-Aug-1996
ACCESSIONS B28044
REFERENCE  A94179
  #authors   Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
  #journal   Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
  #title     Identity of the V-kappa-10 Ars-A gene segments of the A/J and
             BALB/c strains.
  #cross-references MUID:87317629
  #accession B28044
  ##molecule_type mRNA
  ##residues    1-107 ##label MEE
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
SUMMARY       #length 107 #molecular-weight 11738 #checksum 7011

Query Match     100.0%;    Score 51;  DB 7; Length 107;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db        50 ytsrlhs 56
             |||||||
Qy         1 YTSRLHS 7

RESULT     6
ENTRY      B49026        #type complete
TITLE      Ig kappa chain v region, anti-idiotypic monoclonal antibody -
           mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
           25-Oct-1996
ACCESSIONS B49026; PL0220
REFERENCE  A49026
  #authors   Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.;
             Schwartz, R.S.
  #journal   Eur. J. Immunol. (1991) 21:2185-2193
  #title     Molecular heterogeneity of auto-anti-idiotypic antibodies in
             MLR-lpr/lpr mice.
  #cross-references MUID:91364791
  #accession B49026
  ##status      preliminary; not compared with conceptual translation
  ##molecule_type nucleic acid
  ##residues    1-107 ##label KOI
  ##cross-references NCBIP:60876
  ##experimental_source MLR-lpr/lpr
  ##note     sequence extracted from NCBI backbone
REFERENCE  PL0220
  #authors   Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz,
             J.; Barrett, K.J.; Schwartz, R.S.
  #journal   J. Exp. Med. (1990) 171:1919-1930
  #title     An immunoglobulin light chain from a lupus-prone mouse
             induces autoantibodies in normal mice.
  #cross-references MUID:90278348
  #accession PL0220
  ##status      nucleic acid sequence not shown
  ##molecule_type mRNA
  ##residues    1-107 ##label PUC
  ##experimental_source strain lupus-prone MRL-lpr/lpr mouse
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
   24-34          #region complementarity-determining 1\
   50-56          #region complementarity-determining 2\
   89-97          #region complementarity-determining 3
```

```
SUMMARY           #length 107 #molecular-weight 11859 #checksum 8401

Query Match
Best Local Similarity 100.0%;   Score 51;  DB 7;  Length 107;
                                          Pred. No. 2.38e-01;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      50 ytsrlhs 56
           |||||||
Qy       1 YTSRLHS 7

RESULT            7
ENTRY             A28044     #type complete
TITLE             Ig kappa chain v region (22B5) - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              19-May-1989 #sequence_revision 19-May-1989 #text_change
                  16-Aug-1996
ACCESSIONS        A28044
REFERENCE         A94179
  #authors        Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
  #journal        Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
  #title          Identity of the V-kappa-10-Ars-A gene segments of the A/J and
                  BALB/c strains.
  #cross-references MUID:87317629
  #accession      A28044
  ##molecule_type mRNA
  ##residues      1-107 ##label MEE
CLASSIFICATION    #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          heterotetramer; immunoglobulin
SUMMARY           #length 107 #molecular-weight 11832 #checksum 7241

Query Match
Best Local Similarity 100.0%;   Score 51;  DB 7;  Length 107;
                                          Pred. No. 2.38e-01;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      50 ytsrlhs 56
           |||||||
Qy       1 YTSRLHS 7

RESULT            8
ENTRY             C48677     #type fragment
TITLE             Ig light chain V-J region (419.1) - mouse (fragment)
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              19-May-1994 #sequence_revision 19-May-1994 #text_change
                  16-Aug-1996
ACCESSIONS        C48677
REFERENCE         A48677
  #authors        Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
                  P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
  #journal        Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
  #title          Molecular characterization of monoclonal CRI-A-positive
                  anti-arsonate antibodies derived from idiotype-negative
                  mice bearing a light chain polymorphism.
  #accession      C48677
  ##status        preliminary; not compared with conceptual translation
  ##molecule_type mRNA
  ##residues      1-107 ##label TAS
CLASSIFICATION    #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          immunoglobulin
SUMMARY           #length 107 #checksum 7315

Query Match
Best Local Similarity 100.0%;   Score 51;  DB 7;  Length 107;
                                          Pred. No. 2.38e-01;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      50 ytsrlhs 56
           |||||||
Qy       1 YTSRLHS 7

RESULT            9
ENTRY             D48677     #type fragment
TITLE             Ig light chain V-J region (24) - mouse (fragment)
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              19-May-1994 #sequence_revision 19-May-1994 #text_change
                  16-Aug-1996
ACCESSIONS        D48677
REFERENCE         A48677
  #authors        Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
                  P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
  #journal        Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
  #title          Molecular characterization of monoclonal CRI-A-positive
                  anti-arsonate antibodies derived from idiotype-negative
                  mice bearing a light chain polymorphism.
  #accession      D48677
  ##status        preliminary; not compared with conceptual translation
  ##molecule_type mRNA
  ##residues      1-107 ##label TAS
CLASSIFICATION    #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          immunoglobulin
SUMMARY           #length 107 #checksum 7155

Query Match
Best Local Similarity 100.0%;   Score 51;  DB 7;  Length 107;
                                          Pred. No. 2.38e-01;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      50 ytsrlhs 56
           |||||||
Qy       1 YTSRLHS 7

RESULT            10
ENTRY             S69902     #type complete
TITLE             Ig kappa light chain (clone KL2.28) - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
                  09-May-1997
ACCESSIONS        S69902
REFERENCE         S69900
  #authors        Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
  #journal        Immunology (1992) 75:116-121
  #title          B-cell proliferation initiated by Ia cross-linking and
                  sustained by interleukins leads to class switching but not
                  somatic mutation in vitro.
  #accession      S69902
  ##status        preliminary; translation not shown
  ##molecule_type DNA
  ##residues      1-108 ##label WYS
  ##cross-references EMBL:X55043
CLASSIFICATION    #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY           #length 108 #molecular-weight 11895 #checksum 1228

Query Match
Best Local Similarity 100.0%;   Score 51;  DB 7;  Length 108;
                                          Pred. No. 2.38e-01;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      50 ytsrlhs 56
           |||||||
Qy       1 YTSRLHS 7

RESULT            11
ENTRY             S69903     #type complete
TITLE             Ig kappa light chain (clone KL2.29) - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
                  09-May-1997
ACCESSIONS        S69903
REFERENCE         S69900
  #authors        Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
  #journal        Immunology (1992) 75:116-121
  #title          B-cell proliferation initiated by Ia cross-linking and
                  sustained by interleukins leads to class switching but not
                  somatic mutation in vitro.
  #accession      S69903
```

```
                        #description  Production and cloning of TMV-specific monoclonal antibodies.
                        #accession    S38862
                        ##status      preliminary
                        ##molecule_type mRNA
                        ##residues    1-108 ##label FIS
                        ##cross-references EMBL:X75854
CLASSIFICATION          #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS                heterotetramer; immunoglobulin
SUMMARY                 #length 108 #molecular-weight 11865 #checksum 1422

Query Match             100.0%;  Score 51;  DB 7;  Length 108;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db       50 ytsrlhs 56
            |||||||
Qy        1 YTSRLHS 7


RESULT   14
ENTRY    S69900       #type complete
TITLE    Ig kappa light chain (clone KL2.18) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
         09-May-1997
ACCESSIONS A01927
REFERENCE  S69900
         #authors   Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
         #journal   Immunology (1992) 75:116-121
         #title     B-cell proliferation initiated by Ia cross-linking and
                    sustained by interleukins leads to class switching but not
                    somatic mutation in vitro.
         #accession S69900
         ##status   preliminary; translation not shown
         ##molecule_type DNA
         ##residues 1-108 ##label WYS
         ##cross-references EMBL:X55041
CLASSIFICATION          #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY                 #length 108 #molecular-weight 11954 #checksum 1768

Query Match             100.0%;  Score 51;  DB 7;  Length 108;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db       50 ytsrlhs 56
            |||||||
Qy        1 YTSRLHS 7


RESULT   15
ENTRY    S19970       #type fragment
TITLE    Ig kappa chain v region (M-T151) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
         16-Aug-1996
ACCESSIONS S19970
REFERENCE  S19963
         #authors   Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
         #submission submitted to the EMBL Data Library, March 1992
         #description Structural characterization of CD4 mAb.
         #accession S19970
         ##status   preliminary
         ##molecule_type mRNA
         ##residues 1-108 ##label WEI
         ##cross-references EMBL:X65095
CLASSIFICATION          #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS                heterotetramer; immunoglobulin
SUMMARY                 #length 108 #checksum 2135

Query Match             100.0%;  Score 51;  DB 7;  Length 108;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
                        ##status      preliminary; translation not shown
                        ##molecule_type DNA
                        ##residues    1-108 ##label WYS
                        ##cross-references EMBL:X55044
CLASSIFICATION          #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY                 #length 108 #molecular-weight 11931 #checksum 1846

Query Match             100.0%;  Score 51;  DB 7;  Length 108;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db       50 ytsrlhs 56
            |||||||
Qy        1 YTSRLHS 7


RESULT   12
ENTRY    KVMSAR       #type complete
TITLE    Ig kappa chain v regions (anti-arsonate hybridoma proteins) -
         mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change
         16-Aug-1996
ACCESSIONS A01927
REFERENCE  A01927
         #authors   Siegelman, M.; Capra, J.D.
         #journal   Proc. Natl. Acad. Sci. U.S.A. (1981) 78:7679-7683
         #title     Complete amino acid sequence of light chain variable regions
                    derived from five monoclonal anti-p-azophenylarsonate
                    antibodies differing with respect to a crossreactive
                    idiotype.
         #cross-references MUID:82150934
         #accession A01927
         ##molecule_type protein
         ##residues 1-108 ##label SIE
         ##experimental_source strain A/J
         ##note     HP 93G7 differs in having 93-Met; HP 123E6 differs in
                    having 7-Ser, 92-Tyr, and 93-Met; HP 124E1 differs in
                    having 30-Asn, 92-Lys, and 93-Thr; and HP 91A3 differs
                    in having 8-Pro, 30-Asn, 37-Arg, 84-Ser, and 93-Ala
COMMENT  The sequence shown is HP R16.7.
COMPLEX  An immunoglobulin heterotetramer subunit consists of two
         identical light (kappa or lambda) and two identical heavy
         (alpha, delta, epsilon, gamma, or mu) chains usually
         stabilized by interchain disulfide bonds. In some cases,
         such as IgA and IgM, the subunits associate into larger
         oligomers.
CLASSIFICATION          #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS                heterotetramer
FEATURE
         23-88          #disulfide_bonds #status predicted
SUMMARY                 #length 108 #molecular-weight 11910 #checksum 1537

Query Match             100.0%;  Score 51;  DB 2;  Length 108;
Best Local Similarity 100.0%;    Pred. No. 2.38e-01;
Matches     7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db       50 ytsrlhs 56
            |||||||
Qy        1 YTSRLHS 7


RESULT   13
ENTRY    S38862       #type complete
TITLE    Ig kappa chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
         16-Aug-1996
ACCESSIONS S38862
REFERENCE  S37200
         #authors   Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.;
                    Kreuzaler, F.
         #submission submitted to the EMBL Data Library, August 1993
```

```
Db    50 ytsrlhs 56
      |||||||
Qy     1 YTSRLHS 7

RESULT   16
ENTRY          PH0888      #type fragment
TITLE          Ig light chain V region (anti-CD3) - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
               16-Aug-1996
ACCESSIONS     PH0888
REFERENCE      PH0885
#authors       Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.;
               Beverley, P.C.L.; Feldmann, M.; Carter, P.
#journal       J. Exp. Med. (1992) 175:217-225
#title         Development of humanized bispecific antibodies reactive with
               cytotoxic lymphocytes and tumor cells overexpressing the
               HER2 protooncogene.
#cross-references MUID:92113462
#accession     PH0888
##molecule_type mRNA
##residues     1-109 ##label SHA
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS       immunoglobulin
SUMMARY        #length 109  #checksum 4838

Query Match    100.0%;  Score 51;  DB 7;  Length 109;
Best Local Similarity 100.0%;  Pred. No. 2.38e-01;
Matches     7;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    50 ytsrlhs 56
      |||||||
Qy     1 YTSRLHS 7

RESULT   17
ENTRY          A53276      #type complete
TITLE          Ig kappa chain V region - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           02-May-1994 #sequence_revision 18-Nov-1994 #text_change
               16-Aug-1996
ACCESSIONS     A53276
REFERENCE      A53276
#authors       Kim, S.O.; Sanz, I.; Williams, C.; Capra, J.D.; Gottlieb,
               P.D.
#journal       Immunogenetics (1991) 34:231-241
#title         Polymorphism in V kappa 10 genes encoding L chains of
               antibodies bearing the Ars-A and A48 cross-reactive
               idiotypes.
#cross-references MUID:92010099
#accession     A53276
##status       preliminary
##molecule_type DNA
##residues     1-115 ##label KIM
##cross-references NCBIN:62777; NCBIP:62780
##experimental_source AJ1 strain
##note         sequence extracted from NCBI backbone
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 115  #molecular-weight 12681  #checksum 7342

Query Match    100.0%;  Score 51;  DB 7;  Length 115;
Best Local Similarity 100.0%;  Pred. No. 2.38e-01;
Matches     7;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    70 ytsrlhs 76
      |||||||
Qy     1 YTSRLHS 7

RESULT   18
ENTRY          JL0080      #type fragment
```

```
TITLE          Ig light chain precursor V region (anti-phenyloxazolone,
               18C10) - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
               06-Dec-1996
ACCESSIONS     JL0080
REFERENCE      JL0076
#authors       Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
#journal       Mol. Immunol. (1988) 25:859-865
#title         Combinatorial association of V genes: one VH gene codes for
               three non-cross-reactive monoclonal antibodies each
               specific for a different antigen (phOxazolone, NP or GAT).
#cross-references MUID:8096973
#accession     JL0080
##molecule_type mRNA
##residues     1-115 ##label KAA
##note         the authors translated the codon AGG for residue 30 as
               Ser
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS       immunoglobulin
FEATURE
1-6            #domain signal sequence (fragment) #status predicted
               #label SIG\
7-115          #product Ig light chain #status predicted #label MAT\
30-40          #region complementarity-determining 1\
56-62          #region complementarity-determining 2
SUMMARY        #length 115  #checksum 7375

Query Match    100.0%;  Score 51;  DB 7;  Length 115;
Best Local Similarity 100.0%;  Pred. No. 2.38e-01;
Matches     7;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    56 ytsrlhs 62
      |||||||
Qy     1 YTSRLHS 7

RESULT   19
ENTRY          A29380      #type fragment
TITLE          Ig kappa chain precursor V region (AC-1001) - mouse
               (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
               16-Aug-1996
ACCESSIONS     A29380
REFERENCE      A92612
#authors       Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
#journal       J. Biol. Chem. (1987) 262:13579-13583
#title         Nucleotide and translated amino acid sequences of cDNA coding
               for the variable regions of the light and heavy chains of
               mouse hybridoma antibodies to blood group A and B
               substances.
#cross-references MUID:88007582
#accession     A29380
##molecule_type mRNA
##residues     1-122 ##label CHE
##note         the authors translated the codon TTC for residue 1 as
               Leu
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 122  #checksum 9064

Query Match    100.0%;  Score 51;  DB 7;  Length 122;
Best Local Similarity 100.0%;  Pred. No. 2.38e-01;
Matches     7;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    64 ytsrlhs 70
      |||||||
Qy     1 YTSRLHS 7

RESULT   20
ENTRY          PH1224      #type fragment
```

```
TITLE          Ig kappa chain precursor V region (M-T151) - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
               16-Aug-1996
ACCESSIONS     PH1224
REFERENCE      PH1224
  #authors     Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.;
               Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber,
               E.P.; Riethmueller, G.; Weidle, U.H.
  #journal     Gene (1992) 121:271-278
  #title       Combinatorial functions of two chimeric antibodies directed
               to human CD4 and one directed to the alpha-chain of the
               human interleukin-2 receptor.
  #accession   PH1224
  ##molecule_type mRNA
  ##residues   1-127 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE
  1-20         #domain signal sequence #status predicted #label SIG\
  21-127       #product Ig light chain V region #status predicted
               #label MAT
SUMMARY        #length 127 #checksum 4396

Query Match    100.0%; Score 51; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.38e-01;
  Matches    7; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Db    70 ytsrlhs 76
         |||||||
Qy     1 YTSRLHS 7


RESULT   21
ENTRY          A26406       #type complete
TITLE          Ig kappa chain V region (Ars-A) - mouse
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change
               16-Aug-1996
ACCESSIONS     A26406
REFERENCE      A26406
  #authors     Sanz, I.; Capra, J.D.
  #journal     Proc. Natl. Acad. Sci. U.S.A. (1987) 84:1085-1089
  #title       V-K and J-K gene segments of A/J Ars-A antibodies: somatic
               recombination generates the essential arginine at the
               junction of the variable and joining regions.
  #cross-references MUID:87147197
  #accession   A26406
  ##molecule_type DNA
  ##residues   1-128 ##label SAN
  ##cross-references GB:M15519
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 128 #molecular-weight 14078 #checksum 4901

Query Match    100.0%; Score 51; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.38e-01;
  Matches    7; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Db    70 ytsrlhs 76
         |||||||
Qy     1 YTSRLHS 7


Search completed: Tue Mar  3 14:32:31 1998
Job time : 16 secs.
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 3 11:20:10 1998; MasPar time 1.99 Seconds
                                        74.523 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117D-118
Description: (1-7) from US08137117D.pep
Perfect Score: 51
Sequence: 1 YTSRLHS 7

Scoring table: PAM 150
                  Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
                  Listing first 45 summaries

Database: swiss-prot34
                  1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                  8:part8 9:part9 10:part10 11:part11

Statistics: Mean 21.579; Variance 20.158; scale 1.070

  Pred. No. is the number of results predicted by chance to have a
  score greater than or equal to the score of the result being printed,
  and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	51	100.0	108	5	KV5M_MOUSE	IG KAPPA CHAIN V-V RE	3.04e-02
2	51	100.0	108	5	KV5N_MOUSE	IG KAPPA CHAIN V-V RE	3.04e-02
3	51	100.0	108	5	KV5L_MOUSE	IG KAPPA CHAIN V-V RE	3.04e-02
4	51	100.0	108	5	KV5K_MOUSE	IG KAPPA CHAIN V-V RE	3.04e-02
5	51	100.0	108	5	KV5O_MOUSE	IG KAPPA CHAIN V-V RE	3.04e-02
6	51	100.0	108	5	KV5U_MOUSE	IG KAPPA CHAIN V-V RE	3.04e-02
7	48	94.1	861	7	POLG_FMDVS	GENOME POLYPROTEIN (C	2.05e-01
8	48	94.1	2332	7	POLG_FMDVO	GENOME POLYPROTEIN (N	2.05e-01
9	48	94.1	2332	7	POLG_FMDVA	GENOME POLYPROTEIN (N	2.05e-01
10	48	94.1	2333	7	POLG_FMDV1	GENOME POLYPROTEIN (N	2.05e-01
11	45	88.2	2336	7	POLG_FMDVZ	GENOME POLYPROTEIN (N	1.28e+00
12	44	86.3	178	6	MYCB_RAT	B-MYC TRANSFORMING PR	2.32e+00
13	44	86.3	502	5	K2C8_XENLA	KERATIN, TYPE II CYTO	2.32e+00
14	43	84.3	942	3	KDGD_HUMAN	DIACYLGLYCEROL KINASE	4.14e+00
15	42	82.4	334	3	FEUB_BACSU	IRON-UPTAKE SYSTEM PR	7.32e+00
16	42	82.4	552	10	VNS1_EHDV2	NONSTRUCTURAL PROTEIN	7.32e+00
17	42	82.4	721	11	YIJ1_YEAST	HYPOTHETICAL 84.0 KD	7.32e+00
18	42	82.4	787	11	YFI3_YEAST	HYPOTHETICAL 90.9 KD	7.32e+00
19	42	82.4	960	3	FGD1_MOUSE	PUTATIVE RHO/RAC GUAN	7.32e+00
20	42	82.4	961	3	FGD1_HUMAN	PUTATIVE RHO/RAC GUAN	7.32e+00
21	41	80.4	108	5	KV5J_MOUSE	IG KAPPA CHAIN V-V RE	1.28e+01
22	41	80.4	226	6	MYOG_COTJA	MYOGENIC FACTOR 2 (MY	1.28e+01
23	41	80.4	348	1	AROH_ECOLI	PHOSPHO-2-DEHYDRO-3-D	1.28e+01
24	41	80.4	425	4	FTSA_HAEIN	CELL DIVISION PROTEIN	1.28e+01
25	41	80.4	665	7	NUC2_SCHPO	NUCLEAR SCAFFOLD-LIKE	1.28e+01
26	40	78.4	210	7	OBA5_DROME	PUTATIVE ODORANT-BIND	2.21e+01
27	40	78.4	323	9	SOPB_ECOLI	SOPB PROTEIN (PROTEIN	2.21e+01
28	40	78.4	536	3	DIT1_YEAST	SPORE WALL MATURATION	2.21e+01
29	40	78.4	593	8	PTN9_HUMAN	PROTEIN-TYROSINE PHOS	2.21e+01
30	40	78.4	603	7	PRIM_BACSU	DNA PRIMASE (EC 2.7.7	2.21e+01
31	40	78.4	706	1	BCL6_HUMAN	B-CELL LYMPHOMA 6 PRO	2.21e+01
32	40	78.4	707	1	BCL6_MOUSE	B-CELL LYMPHOMA 6 PRO	2.21e+01
33	40	78.4	798	4	HEPA_HCMVA	DNA HELICASE/PRIMASE	2.21e+01
34	40	78.4	1249	9	TPP2_HUMAN	TRIPEPTIDYL-PEPTIDASE	2.21e+01
35	40	78.4	1942	11	YY05_HUMAN	HYPOTHETICAL MYELOID	2.21e+01
36	39	76.5	152	10	VE1_FPVL	REPLICATION PROTEIN E	3.77e+01
37	39	76.5	309	3	ER25_YEAST	C-4 STEROL METHYL OXI	3.77e+01
38	39	76.5	323	8	RBSC_BACSU	RIBOSE TRANSPORT SYST	3.77e+01
39	39	76.5	335	8	RPOA_PINTH	DNA-DIRECTED RNA POLY	3.77e+01
40	39	76.5	805	10	UBP5_YEAST	UBIQUITIN CARBOXYL-TE	3.77e+01
41	39	76.5	839	6	NI96_YEAST	96 KD NUCLEOPORIN-INT	3.77e+01
42	39	76.5	932	10	VGLB_HSVBC	GLYCOPROTEIN I PRECUR	3.77e+01
43	39	76.5	966	10	V1A_BBMV	1A PROTEIN (CONTAINS:	3.77e+01
44	39	76.5	1639	6	LMG1_DROME	LAMININ GAMMA-1 CHAIN	3.77e+01
45	39	76.5	2505	3	FAS_RAT	FATTY ACID SYNTHASE (	3.77e+01

ALIGNMENTS

RESULT 1
ID   KV5M_MOUSE   STANDARD;   PRT;   108 AA.
AC   P01646;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 123E6).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RA   SIEGELMAN M., CAPRA J.D.;
RX   MEDLINE; 82150934.
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   108   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11989 MW;   23B8BB67 CRC32;

Query Match   100.0%;   Score 51; DB 5; Length 108;
Best Local Similarity 100.0%;   Pred. No. 3.04e-02;
Matches   7;   Conservative   0;   Mismatches 0;   Indels 0;   Gaps 0;

Db   50 ytsrlhs 56
         |||||||
Qy   1 YTSRLHS 7

RESULT 2
ID   KV5N_MOUSE   STANDARD;   PRT;   108 AA.
AC   P01647;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
```

```
DE   IG KAPPA CHAIN V-V REGION (HP 124E1).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN-A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN       1      23   FRAMEWORK 1.
FT   DOMAIN      24      34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      35      49   FRAMEWORK 2.
FT   DOMAIN      50      56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      57      88   FRAMEWORK 3.
FT   DOMAIN      89      97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      98     108   FRAMEWORK 4.
FT   DISULFID    23      88   BY SIMILARITY.
FT   NON_TER    108     108
SQ   SEQUENCE   108 AA;   11965 MW;   84754175 CRC32;

Query Match             100.0%;  Score 51;  DB 5;  Length 108;
Best Local Similarity 100.0%;  Pred. No. 3.04e-02;
Matches       7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db       50 ytsrlhs 56
            |||||||
Qy        1 YTSRLHS 7

RESULT   3
ID   KV5L_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01645;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 93G7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN-A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN       1      23   FRAMEWORK 1.
FT   DOMAIN      24      34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      35      49   FRAMEWORK 2.
FT   DOMAIN      50      56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      57      88   FRAMEWORK 3.
FT   DOMAIN      89      97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      98     108   FRAMEWORK 4.
FT   DISULFID    23      88   BY SIMILARITY.
FT   NON_TER    108     108
SQ   SEQUENCE   108 AA;   11954 MW;   A203E130 CRC32;

Query Match             100.0%;  Score 51;  DB 5;  Length 108;
Best Local Similarity 100.0%;  Pred. No. 3.04e-02;
Matches       7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db       50 ytsrlhs 56
            |||||||
Qy        1 YTSRLHS 7

RESULT   4
ID   KV5K_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01644;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP R16.7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN-A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN       1      23   FRAMEWORK 1.
FT   DOMAIN      24      34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      35      49   FRAMEWORK 2.
FT   DOMAIN      50      56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      57      88   FRAMEWORK 3.
FT   DOMAIN      89      97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      98     108   FRAMEWORK 4.
FT   DISULFID    23      88   BY SIMILARITY.
FT   NON_TER    108     108
SQ   SEQUENCE   108 AA;   11910 MW;   64A62905 CRC32;

Query Match             100.0%;  Score 51;  DB 5;  Length 108;
Best Local Similarity 100.0%;  Pred. No. 3.04e-02;
Matches       7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db       50 ytsrlhs 56
            |||||||
Qy        1 YTSRLHS 7

RESULT   5
ID   KV5Q_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01648;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 91A3).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN-A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN       1      23   FRAMEWORK 1.
FT   DOMAIN      24      34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      35      49   FRAMEWORK 2.
FT   DOMAIN      50      56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      57      88   FRAMEWORK 3.
FT   DOMAIN      89      97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      98     108   FRAMEWORK 4.
FT   DISULFID    23      88   BY SIMILARITY.
FT   NON_TER    108     108
SQ   SEQUENCE   108 AA;   11961 MW;   5B067780 CRC32;

Query Match             100.0%;  Score 51;  DB 5;  Length 108;
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Best Local Similarity 100.0%;   Pred. No. 3.04e-02;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   50 ytsrlhs 56
           |||||||
Qy   1 YTSRLHS 7

RESULT   6
ID   KV5U_MOUSE   STANDARD;   PRT;   108 AA.
AC   P04946;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (NQ5-89.4).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83271467.
RA   KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
RL   NATURE 304:320-324(1983).
CC   -!- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
DR   EMBL; K00745; GI96455; -.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11866 MW; D396F142 CRC32;

Query Match   100.0%; Score 51; DB 5; Length 108;
Best Local Similarity 100.0%;   Pred. No. 3.04e-02;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   50 ytsrlhs 56
           |||||||
Qy   1 YTSRLHS 7

RESULT   7
ID   POLG_FMDVS   STANDARD;   PRT;   861 AA.
AC   P03311;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (COAT PROTEINS VP3, VP1; CORE PROTEIN P52, PROTEASE
DE   (EC 3.4.22.-); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)) (FRAGMENTS).
OS   FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1-SANTA PAU [C-S8]) (APHTHOVIRUS
OS   C).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN   [1]
RP   SEQUENCE OF 1-332 FROM N.A.
RX   MEDLINE; 84005890.
RA   VILLANUEVA N., DAVILA M., ORTIN J., DOMINGO E.;
RL   GENE 23:185-194(1983).
RN   [2]
RP   SEQUENCE OF 333-861 FROM N.A.
RX   MEDLINE; 85286357.
RA   MARTINEZ-SALAS E., ORTIN J., DOMINGO E.;
RL   GENE 35:55-61(1985).
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC   EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC   VP3, AND VP4.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

DR   EMBL; M11027; G210477; -.
DR   PIR; A03913; A03913.
DR   PIR; A24031; A24031.
DR   HSSP; P13899; 1FMD.
KW   POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW   HYDROLASE; THIOL PROTEASE.
FT   NON_TER   1   1
FT   CHAIN   1   46   COAT PROTEIN VP3.
FT   CHAIN   47   254   COAT PROTEIN VP1.
FT   CHAIN   255   332   CORE PROTEIN P52.
FT   NON_CONS   332   333
FT   CHAIN   333   391   PROTEASE.
FT   CHAIN   392   861   RNA-DEPENDENT RNA POLYMERASE.
SQ   SEQUENCE   861 AA; 95554 MW; 1CBC4098 CRC32;

Query Match   94.1%; Score 48; DB 7; Length 861;
Best Local Similarity 85.7%;   Pred. No. 2.05e-01;
Matches   6; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   472 yasrlhs 478
           |:||||||
Qy   1 YTSRLHS 7

RESULT   8
ID   POLG_FMDVO   STANDARD;   PRT;   2332 AA.
AC   P03305;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE   VP4; CORE PROTEINS P12, P34, P14; GENOME-LINKED PROTEIN VPG; PROTEASE
DE   (EC 3.4.22.-); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)).
OS   FOOT-AND-MOUTH DISEASE VIRUS (STRAINS O1K AND O1BFS) (APHTHOVIRUS O).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O1K;
RX   MEDLINE; 84297249.
RA   FORSS S., STREBEL K., BECK E., SCHALLER H.;
RL   NUCLEIC ACIDS RES. 12:6587-6601(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O1BFS;
RX   MEDLINE; 83143292.
RA   MAKOFF A.J., PAYNTER C.A., ROWLANDS D.J., BOOTHROYD J.C.;
RL   NUCLEIC ACIDS RES. 10:8285-8295(1982).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE; 89143740.
RA   ACHARYA R., FRY E., STUART D., FOX G., ROWLANDS D., BROWN F.;
RL   NATURE 337:709-716(1989).
CC   -!- THE STRAIN O1K SEQUENCE IS SHOWN.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- THE COAT PROTEIN VP1 CONTAINS THE MAIN ANTIGENIC DETERMINANTS OF
CC   THE VIRION; THEREFORE, CHANGES IN ITS SEQUENCE MUST BE
CC   RESPONSIBLE FOR THE HIGH ANTIGENIC VARIABILITY OF THE VIRUS.
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC   EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC   VP3, AND VP4.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
DR   EMBL; X00871; G61078; -.
DR   EMBL; J02185; G210436; -.
DR   PIR; A03907; GNNYF.
DR   HSSP; P08544; 1BBT.
KW   POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW   HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT   CHAIN   1   201   NONSTRUCTURAL PROTEIN P20A.
FT   CHAIN   202   286   COAT PROTEIN VP4.
FT   CHAIN   287   504   COAT PROTEIN VP2.
FT   CHAIN   505   724   COAT PROTEIN VP3.
FT   CHAIN   725   937   COAT PROTEIN VP1.
FT   CHAIN   938   1107   CORE PROTEIN P12.

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FT   CHAIN          1108   1425        CORE PROTEIN P34.
FT   CHAIN          1426   1578        CORE PROTEIN P14.
FT   CHAIN          1579   1649        GENOME-LINKED PROTEIN VPG.
FT   CHAIN          1650   1862        PROTEASE.
FT   CHAIN          1863   2332        RNA-DIRECTED RNA POLYMERASE.
FT   LIPID           202    202        MYRISTATE.
FT   DISULFID        511    511        INTERCHAIN  (IN VP3 DIMER).
FT   DISULFID        406    858        IN VP2-VP1 DIMER.
FT   VARIANT         780    780        I -> V (IN STRAIN O1BFS).
FT   VARIANT         808    808        G -> R (IN STRAIN O1BFS).
FT   VARIANT         861    861        N -> S (IN STRAIN O1BFS).
SQ   SEQUENCE       2332 AA;  258924 MW;  251F5647 CRC32;

Query Match             94.1%;  Score 48;  DB 7;  Length 2332;
Best Local Similarity   85.7%;  Pred. No. 2.05e-01;
    Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db      1943 yasrlhs 1949
             |:|||||
Qy         1 YTSRLHS 7


RESULT    9
ID   POLG_FMDVA      STANDARD;        PRT;   2332 AA.
AC   P03308; P03312;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE   VP4; CORE PROTEINS X, P14, P41, P19; GENOME-LINKED PROTEINS VPG1 TO
DE   VPG3; PICORNAIN 3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED
DE   RNA POLYMERASE (EC 2.7.7.48)).
OS   FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12) (APHTHOVIRUS A).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85211015.
RA   ROBERTSON B.H., GRUBMAN M.J., WEDDELL G.N., MOORE D.M., WELSH J.D.,
RA   FISCHER T., DOWBENKO D.J., YANSURA D.G., SMALL B., KLEID D.G.;
RL   J. VIROL. 54:651-660(1985).
RN   [2]
RP   SEQUENCE OF 1863-2332 FROM N.A.
RX   MEDLINE; 83225513.
RA   ROBERTSON B.H., MORGAN D.O., MOORE D.M., GRUBMAN M.J., CARD J.,
RA   FISCHER T., WEDDELL G.N., DOWBENKO D.J., YANSURA D.G.;
RL   VIROLOGY 126:614-623(1983).
RN   [3]
RP   SEQUENCE OF 715-955 FROM N.A.
RX   MEDLINE; 82061853.
RA   KLEID D.G., YANSURA D.G., SMALL B., DOWBENKO D.J., MOORE D.M.,
RA   GRUBMAN M.J., MCKERCHER P.D., MORGAN D.O., ROBERTSON B.H.;
RL   SCIENCE 214:1125-1129(1981).
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
DR   EMBL; M10975; G210307; -.
DR   EMBL; M10975; E807; -.
DR   EMBL; J02187; G210548; -.
DR   PIR; A25794; GNNY4F.
DR   HSSP; P08544; 1BBT.
KW   POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW   HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT   CHAIN            1    200        NONSTRUCTURAL PROTEIN P20A.
FT   CHAIN          201    285        COAT PROTEIN VP4.
FT   CHAIN          286    503        COAT PROTEIN VP2.
FT   CHAIN          504    723        COAT PROTEIN VP3.
FT   CHAIN          724    937        COAT PROTEIN VP1.
FT   CHAIN          938    953        CORE PROTEIN X.
FT   CHAIN          954   1107        CORE PROTEIN P14.
FT   CHAIN         1108   1425        CORE PROTEIN P41.
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FT   CHAIN          1426   1578        CORE PROTEIN P19.
FT   CHAIN          1579   1601        GENOME-LINKED PROTEIN VPG1.
FT   CHAIN          1602   1625        GENOME-LINKED PROTEIN VPG2.
FT   CHAIN          1626   1649        GENOME-LINKED PROTEIN VPG3.
FT   CHAIN          1650   1862        PROTEASE.
FT   CHAIN          1863   2332        RNA-DIRECTED RNA POLYMERASE.
FT   LIPID           201    201        MYRISTATE.
SQ   SEQUENCE       2332 AA;  259408 MW;  BDF68BA5 CRC32;

Query Match             94.1%;  Score 48;  DB 7;  Length 2332;
Best Local Similarity   85.7%;  Pred. No. 2.05e-01;
    Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db      1943 yasrlhs 1949
             |:|||||
Qy         1 YTSRLHS 7


RESULT    10
ID   POLG_FMDV1      STANDARD;        PRT;   2333 AA.
AC   P03306;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE   VP4; CORE PROTEIN P52; GENOME-LINKED PROTEINS VPG1 TO VPG3; PICORNAIN
DE   3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE
DE   (EC 2.7.7.48)).
OS   FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A10-61) (APHTHOVIRUS A).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84165947.
RA   CARROLL A.R., ROWLANDS D.J., CLARKE B.E.;
RL   NUCLEIC ACIDS RES. 12:2461-2472(1984).
RN   [2]
RP   SEQUENCE OF 115-1048 FROM N.A.
RX   MEDLINE; 82211814.
RA   BOOTHROYD J.C., HARRIS T.J.R., ROWLANDS D.J., LOWE P.A.;
RL   GENE 17:153-161(1982).
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
DR   EMBL; V01130; G61049; -.
DR   EMBL; X00429; G61064; -.
DR   PIR; A03908; GNNY2F.
DR   HSSP; P08544; 1BBT.
KW   POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW   HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT   CHAIN            1    201        NONSTRUCTURAL PROTEIN P20A.
FT   CHAIN          202    286        COAT PROTEIN VP4.
FT   CHAIN          287    504        COAT PROTEIN VP2.
FT   CHAIN          505    725        COAT PROTEIN VP3.
FT   CHAIN          726    937        COAT PROTEIN VP1.
FT   CHAIN          938   1578        CORE PROTEIN P52.
FT   CHAIN         1579   1601        GENOME-LINKED PROTEIN VPG1.
FT   CHAIN         1602   1625        GENOME-LINKED PROTEIN VPG2.
FT   CHAIN         1626   1649        GENOME-LINKED PROTEIN VPG3.
FT   CHAIN         1650   1863        PROTEASE P20B.
FT   CHAIN         1864   2333        RNA-DIRECTED RNA POLYMERASE P56A.
FT   LIPID          202    202        MYRISTATE.
FT   CONFLICT       396    396        S -> C (IN REF. 2).
FT   CONFLICT       632    632        P -> L (IN REF. 2).
SQ   SEQUENCE       2333 AA;  259645 MW;  7BF32432 CRC32;

Query Match             94.1%;  Score 48;  DB 7;  Length 2333;
Best Local Similarity   85.7%;  Pred. No. 2.05e-01;
    Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Db      1944 yasrlhs 1950
             |:|||||
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Qy   1 YTSRLHS 7

RESULT 11
ID POLG_FMDVZ   STANDARD;   PRT;   2336 AA.
AC P49303;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE VP4; CORE PROTEINS X, P14, P41, P19; GENOME-LINKED PROTEINS VPG1 TO
DE VPG3; PICORNAIN 3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED
DE RNA POLYMERASE (EC 2.7.7.48)).
OS FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A22/550 AZERBAIJAN 65)
OS (APHTHOVIRUS A).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RA SOSNOVTSEV S.V., ONISCHENKO A.M., PETROV N.A., KALASHNIKOVA T.I.,
RA MAMAEVA N.V., DRYGIN V.Y., PEREVOZCHIKOVA N.A., VASILENKO S.K.;
RL SUBMITTED (AUG-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC   EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC   VP3, AND VP4.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
DR EMBL; X74812; G397966; -.
KW POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT CHAIN   1   201 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN   202   286 COAT PROTEIN VP4.
FT CHAIN   287   504 COAT PROTEIN VP2.
FT CHAIN   505   724 COAT PROTEIN VP3.
FT CHAIN   725   938 COAT PROTEIN VP1.
FT CHAIN   939   954 CORE PROTEIN X.
FT CHAIN   955   1108 CORE PROTEIN P14.
FT CHAIN   1109   1426 CORE PROTEIN P41.
FT CHAIN   1427   1579 CORE PROTEIN P19.
FT CHAIN   1580   1602 GENOME-LINKED PROTEIN VPG1.
FT CHAIN   1603   1626 GENOME-LINKED PROTEIN VPG2.
FT CHAIN   1627   1650 GENOME-LINKED PROTEIN VPG3.
FT CHAIN   1651   1863 PROTEASE.
FT CHAIN   1864   2336 RNA-DIRECTED RNA POLYMERASE.
FT LIPID   202   202 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 2336 AA; 259982 MW; 795073B4 CRC32;

Query Match   88.2%; Score 45; DB 7; Length 2336;
Best Local Similarity   71.4%; Pred. No. 1.28e+00;
Matches   5; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Db   1944 yasrlhn 1950
          |:|||:
Qy   1 YTSRLHS 7

RESULT 12
ID MYCB_RAT   STANDARD;   PRT;   178 AA.
AC P15063;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE B-MYC TRANSFORMING PROTEIN (FRAGMENT).
GN MYCB.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER, AND BRAIN;
RX MEDLINE; 90082428.
RA ASKER C., STEINITZ M., ANDERSSON K., SUEMEGI J., KLEIN G.,
RA INGVARSSON S.;
RL ONCOGENE 4:1523-1527(1989).

RN [2]
RP SEQUENCE OF 1-120 FROM N.A.
RX MEDLINE; 89096904.
RA INGVARSSON S., ASKER C., AXELSON H., KLEIN G., SUEMEGI J.;
RL MOL. CELL. BIOL. 8:3168-3174(1988).
DR EMBL; X17455; G55831; -.
DR EMBL; M21133; -; NOT_ANNOTATED_CDS.
DR PIR; A31198; TVRTBM.
DR PIR; A45502; A45502.
DR PROSITE; PS00038; HELIX_LOOP_HELIX.
DR TRANSFAC; T01563; -.
KW TRANSFORMING PROTEIN; NUCLEAR PROTEIN; DNA-BINDING.
FT NON_TER   178   178
SQ SEQUENCE 178 AA; 19463 MW; 8AEBC433 CRC32;

Query Match   86.3%; Score 44; DB 6; Length 178;
Best Local Similarity   83.3%; Pred. No. 2.32e+00;
Matches   5; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db   160 yasrlh 165
          |:|||:
Qy   1 YTSRLH 6

RESULT 13
ID K2C8_XENLA   STANDARD;   PRT;   502 AA.
AC P08776;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86313601.
RA FRANZ J.K., FRANKE W.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:6475-6479(1986).
CC -!- THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN,
CC   I (ACIDIC) AND II (NEUTRAL TO BASIC) (40-55 AND 56-70 KILODALTONS,
CC   RESPECTIVELY).
CC -!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
CC -!- KERATIN 8 ASSOCIATES WITH KERATIN 18.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED IN THE OOCYTE IN EARLY AND LATE
CC   EMBRYONIC STAGES.
CC -!- SIMILARITY: TO ALL OTHER INTERMEDIATE FILAMENT PROTEINS.
DR EMBL; M13811; G214556; -.
DR PIR; A23547; A23547.
DR PROSITE; PS00226; IF.
KW INTERMEDIATE FILAMENT; COILED COIL; HEPTAD REPEAT PATTERN; KERATIN.
FT DOMAIN   1   98 HEAD.
FT DOMAIN   99   406 ROD.
FT DOMAIN   407   502 TAIL.
FT DOMAIN   99   134 COIL 1A.
FT DOMAIN   135   151 LINKER 1.
FT DOMAIN   152   243 COIL 1B.
FT DOMAIN   244   267 LINKER 12.
FT DOMAIN   268   406 COIL 2.
FT SITE   350   350 STUTTER.
SQ SEQUENCE 502 AA; 55679 MW; 79A4B1D3 CRC32;

Query Match   86.3%; Score 44; DB 5; Length 502;
Best Local Similarity   71.4%; Pred. No. 2.32e+00;
Matches   5; Conservative   2; Mismatches   2; Indels   0; Gaps   0;

Db   321 yttrlqs 327
          |:|||:|
Qy   1 YTSRLHS 7

RESULT 14
ID KDGD_HUMAN .   STANDARD;   PRT;   942 AA.
AC P52824;

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DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   DIACYLGLYCEROL KINASE, DELTA (EC 2.7.1.107) (DIGLYCERIDE KINASE)
DE   (DGK) (80 KD DIACYLGLYCEROL KINASE).
GN   DAGK4.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95331799.
RA   PILZ A., SCHAAP D., HUNT D., FITZGIBBON J.;
RL   GENOMICS 26:599-601(1995).
CC   -!- CATALYTIC ACTIVITY: ATP + 1,2-DIACYLGLYCEROL = ADP +
CC       1,2-DIACYLGLYCEROL 3-PHOSPHATE.
CC   -!- SIMILARITY: CONTAINS 3 COPIES OF THE ZINC-DEPENDENT PHORBOL-
CC       ESTER AND DAG BINDING DOMAIN.
DR   EMBL; L38707; G606757; -.
DR   MIM; 601207; -.
KW   TRANSFERASE; KINASE; PHORBOL-ESTER BINDING; MULTIGENE FAMILY.
FT   DOMAIN        61    108    PHORBOL-ESTER AND DAG BINDING (BY
FT                             SIMILARITY).
FT   DOMAIN       122    168    PHORBOL-ESTER AND DAG BINDING (BY
FT                             SIMILARITY).
FT   DOMAIN       184    234    PHORBOL-ESTER AND DAG BINDING (BY
FT                             SIMILARITY).
SQ   SEQUENCE  942 AA;  101403 MW;  34C318EB CRC32;

Query Match             84.3%;  DB 5; Length 942;
Best Local Similarity   71.4%;  Pred. No. 4.14e+00;
Matches    5; Conservative    5; Mismatches    2; Indels    0; Gaps    0;

Db   769 ftsrlhn 775
         :|||||:
Qy     1 YTSRLHS 7


RESULT  15
ID   FEUB_BACSU    STANDARD;    PRT;   334 AA.
AC   P40410;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   IRON-UPTAKE SYSTEM PROTEIN FEUB.
GN   FEUB.
OS   BACILLUS SUBTILIS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BD99 / MS94;
RX   MEDLINE; 94281248.
RA   QUIRK P.G., GUFFANTI A.A., CLEJAN S., CHENG J., KRULWICH T.A.;
RL   BIOCHIM. BIOPHYS. ACTA 1186:27-34(1994).
CC   -!- FUNCTION: THIS IS ONE OF THE PROTEINS INVOLVED IN AN IRON- UPTAKE
CC       SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE
CC       SUBSTRATE ACROSS THE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: TO OTHER INTEGRAL MEMBRANE PROTEINS INVOLVED IN TONB-
CC       PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE FECCD
CC       SUBFAMILY.
DR   EMBL; L19954; G438459; -.
DR   SUBTILIST; BG10836; FEUB.
DR   PROSITE; PS00402; BPD_TRANSP_INN_MEMBR.
KW   IRON TRANSPORT; TRANSPORT; TRANSMEMBRANE.
FT   TRANSMEM       9     29    POTENTIAL.
FT   TRANSMEM      63     83    POTENTIAL.
FT   TRANSMEM      91    111    POTENTIAL.
FT   TRANSMEM     119    139    POTENTIAL.
FT   TRANSMEM     150    170    POTENTIAL.
FT   TRANSMEM     191    211    POTENTIAL.
FT   TRANSMEM     243    263    POTENTIAL.
FT   TRANSMEM     281    301    POTENTIAL.
FT   TRANSMEM     305    325    POTENTIAL.
SQ   SEQUENCE  334 AA;  35896 MW;  33B73F26 CRC32;

Query Match             82.4%;  DB 3; Length 334;
Best Local Similarity   66.7%;  Pred. No. 7.32e+00;
Matches    4; Conservative    2; Mismatches    0; Indels    0; Gaps    0;

Db   182 ysarlh 187
         |::|||
Qy     1 YTSRLH 6


Search completed: Tue Mar  3 11:20:19 1998
Job time : 9 secs.
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